OM protein - protein search, using sw model

Run on: September 9, 2005, 15:07:04 ; Search time 78 Seconds
(without alignments)
639.642 Million cell updates/sec

Title: US-10-001-245C-36
Perfect score: 692
Sequence: 1 DQVDVKDCANHEIKEVLVPG.....VLGDNGVLACAIATHAKIRD 129

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	692	100.0	129	5	ABG67011	Abg67011 House dus
2	684	98.8	129	5	ABG67013	Abg67013 House dus
3	684	98.8	129	5	ABG67016	Abg67016 House dus
4	683	98.7	129	5	ABG67015	Abg67015 House dus
5	683	98.7	129	5	ABG67014	Abg67014 House dus
6	682	98.6	129	5	ABG67012	Abg67012 House dus
7	657	94.9	129	5	ABG67019	Abg67019 House dus
8	657	94.9	129	5	ABG67022	Abg67022 House dus
9	656	94.8	129	5	ABG67021	Abg67021 House dus
10	656	94.8	129	5	ABG67020	Abg67020 House dus
11	655	94.7	129	5	ABG67018	Abg67018 House dus
12	655	94.7	129	5	ABG67017	Abg67017 House dus
13	648	93.6	129	5	ABG67010	Abg67010 House dus
14	646	93.4	129	5	ABG66996	Abg66996 House dus
15	643	92.9	129	5	ABG66994	Abg66994 House dus
16	642	92.8	129	5	ABG66993	Abg66993 House dus
17	641	92.6	129	5	ABG66992	Abg66992 House dus
18	641	92.6	129	5	ABG67007	Abg67007 House dus
19	641	92.6	129	5	ABG66976	Abg66976 House dus
20	641	92.6	129	5	ABG67006	Abg67006 House dus
21	641	92.6	129	5	ABG67008	Abg67008 House dus
22	640	92.5	129	5	ABG67001	Abg67001 House dus
23	640	92.5	129	5	ABG67003	Abg67003 House dus
24	639	92.3	129	5	ABG66972	Abg66972 House dus
25	639	92.3	129	5	ABG67000	Abg67000 House dus
26	639	92.3	129	5	ABG66974	Abg66974 House dus
27	639	92.3	129	5	ABG67004	Abg67004 House dus
28	638	92.2	129	5	ABG66995	Abg66995 House dus
29	638	92.2	145	5	ABB76047	Abb76047 Dust mite
30	637	92.1	129	5	ABG67002	Abg67002 House dus
31	637	92.1	129	5	ABG66973	Abg66973 House dus
32	635	91.8	129	5	ABG66997	Abg66997 House dus
33	635	91.8	136	8	ADR87228	Adr87228 Dust mite
34	635	91.8	146	2	AAR39360	Aar39360 Dermatoph
35	635	91.8	146	2	AAR51728	Aar51728 Der p II.
36	635	91.8	146	2	AAW71909	Aaw71909 Dermatoph
37	635	91.8	146	2	AAY25581	Aay25581 D. pteron
38	635	91.8	146	2	AAY50357	Aay50357 Dermatoph
39	635	91.8	146	4	AAU18960	Aau18960 House dus
40	635	91.8	146	5	ABG67053	Abg67053 House dus
41	635	91.8	146	6	ABP98483	Abp98483 Amino aci
42	635	91.8	146	7	ADC34831	Adc34831 House dus
43	635	91.8	146	7	ADE38099	Ade38099 European
44	635	91.8	147	2	AAR47064	Aar47064 Protein a
45	633	91.5	129	4	AAU07751	Aau07751 House dus

ALIGNMENTS

RESULT 1
ABG67011
ID ABG67011 standard; protein; 129 AA.
XX
AC ABG67011;
XX
DT 24-SEP-2002 (first entry)
XX
DE House dust mite allergen Der p 2 ALK-G mutant #1.
XX
KW Immunoglobulin E; IgE; allergen; allergy; mutein; hay fever;
KW rhinoconductivitis; rhinitis; asthma; systemic anaphylaxis; mutant;
KW vaccine; antiallergic; B cell epitope.
XX
OS Dermatophagoides pteronyssinus.
OS Synthetic.
XX
PN WO200240676-A2.
XX
PD 23-MAY-2002.
XX
PF 16-NOV-2001; 2001WO-DK000764.
XX
PR 16-NOV-2000; 2000DK-00001718.
PR 16-NOV-2000; 2000US-0249361P.
PR 14-JUN-2001; 2001US-0298170P.
XX
PA (ALKA-) ALK-ABELLO AS.
XX
PI Holm J, Ipsen H, Nedergaard Larsen J, Spangfort MD;
XX
DR WPI; 2002-508328/54.
DR N-PSDB; ABK95627.
XX
PT New recombinant mutant allergen, useful for preventing and/or treating
PT allergy, comprises multiple mutations and reduced immunoglobulin E
PT binding affinity.
XX
PS Example 6; Page; 210pp; English.
XX
CC The invention relates to a recombinant allergen (I) which is a mutant of
CC a naturally occurring allergen, where the mutant allergen has at least
CC four primary mutations, which each reduce the specific immunoglobulin E
CC (IgE) binding capability of the mutated allergen as compared to the IgE
CC binding capability of the naturally occurring allergen, where each
CC primary mutation is a substitution of one surface-exposed amino acid
CC residue with another residue, which does not occur in the same position
CC in the amino acid sequence of any known homologous protein within the

CC taxonomic species from which the naturally occurring allergen originates,
CC and each primary mutation is spaced from each other primary mutation by
CC at least 15 Angstrom , and the primary mutations are placed in such a
CC manner that at least one circular surface region with a area of 800
CC Angstrom ^2 comprises no mutation. Also included are a composition
CC comprising two or more of the recombinant allergens, where the variant
CC allergen is defined by having at least one primary mutation, which is
CC absent in at least one of the other variants, and for each variant no
CC secondary mutation is present within a radius of 15 Angstrom from each
CC absent primary mutation; a DNA sequence encoding the recombinant allergen
CC or its derivative, partial sequence or degenerated sequence, or a
CC sequence which hybridises to it under stringent conditions, where the
CC derivative, partial sequence, degenerated sequence or hybridising
CC sequence encodes a peptide having at least one B cell epitope; an
CC expression vector comprising the DNA and a host cell comprising the
CC vector. The recombinant allergen is useful as a pharmaceutical, for
CC preparing a pharmaceutical for preventing and/or treating allergy, or in
CC a diagnostic assay for assessing relevance, safety or outcome of therapy
CC of a subject, where an IgE containing sample of the subject is mixed with
CC the recombinant allergen and assessed for the level of reactivity between
CC the IgE in the sample and the recombinant allergen. The recombinant
CC allergen or compositions are useful for generating an immune response in
CC a subject, for vaccination or treatment of a subject or for the
CC treatment, prevention or alleviation of allergic reactions in a subject
CC e.g. hay fever, rhinoconductivitis, rhinitis, asthma or systemic
CC anaphylaxis. The present sequence represents a recombinant allergen of
CC the invention. Note: The present sequence was not shown in the
CC specification but was created by the indexer using information in the
CC specification and the corresponding wild-type sequence
XX
SQ Sequence 129 AA;

Query Match 100.0%; Score 692; DB 5; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.3e-73;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120

Qy        121 IATHAKIRD 129
              |||||||||
Db        121 IATHAKIRD 129
```

RESULT 2
ABG67013
ID ABG67013 standard; protein; 129 AA.
XX
AC ABG67013;
XX
DT 24-SEP-2002 (first entry)
XX
DE House dust mite allergen Der p 2 ALK-G mutant #3.
XX
KW Immunoglobulin E; IgE; allergen; allergy; mutein; hay fever;
KW rhinoconductivitis; rhinitis; asthma; systemic anaphylaxis; mutant;
KW vaccine; antiallergic; B cell epitope.
XX
OS Dermatophagoides pteronyssinus.
OS Synthetic.
XX
PN WO200240676-A2.
XX
PD 23-MAY-2002.
XX
PF 16-NOV-2001; 2001WO-DK000764.
XX
PR 16-NOV-2000; 2000DK-00001718.
PR 16-NOV-2000; 2000US-0249361P.
PR 14-JUN-2001; 2001US-0298170P.
XX
PA (ALKA-) ALK-ABELLO AS.
XX
PI Holm J, Ipsen H, Nedergaard Larsen J, Spangfort MD;
XX
DR WPI; 2002-508328/54.
DR N-PSDB; ABK95629.
XX
PT New recombinant mutant allergen, useful for preventing and/or treating
PT allergy, comprises multiple mutations and reduced immunoglobulin E
PT binding affinity.
XX
PS Example 6; Page; 210pp; English.
XX
CC The invention relates to a recombinant allergen (I) which is a mutant of
CC a naturally occurring allergen, where the mutant allergen has at least
CC four primary mutations, which each reduce the specific immunoglobulin E
CC (IgE) binding capability of the mutated allergen as compared to the IgE
CC binding capability of the naturally occurring allergen, where each
CC primary mutation is a substitution of one surface-exposed amino acid
CC residue with another residue, which does not occur in the same position
CC in the amino acid sequence of any known homologous protein within the
CC taxonomic species from which the naturally occurring allergen originates,
CC and each primary mutation is spaced from each other primary mutation by
CC at least 15 Angstrom , and the primary mutations are placed in such a
CC manner that at least one circular surface region with a area of 800
CC Angstrom ^2 comprises no mutation. Also included are a composition
CC comprising two or more of the recombinant allergens, where the variant
CC allergen is defined by having at least one primary mutation, which is
CC absent in at least one of the other variants, and for each variant no
CC secondary mutation is present within a radius of 15 Angstrom from each
CC absent primary mutation; a DNA sequence encoding the recombinant allergen
CC or its derivative, partial sequence or degenerated sequence, or a
CC sequence which hybridises to it under stringent conditions, where the
CC derivative, partial sequence, degenerated sequence or hybridising
CC sequence encodes a peptide having at least one B cell epitope; an
CC expression vector comprising the DNA and a host cell comprising the
CC vector. The recombinant allergen is useful as a pharmaceutical, for
CC preparing a pharmaceutical for preventing and/or treating allergy, or in
CC a diagnostic assay for assessing relevance, safety or outcome of therapy
CC of a subject, where an IgE containing sample of the subject is mixed with
CC the recombinant allergen and assessed for the level of reactivity between
CC the IgE in the sample and the recombinant allergen. The recombinant
CC allergen or compositions are useful for generating an immune response in
CC a subject, for vaccination or treatment of a subject or for the
CC treatment, prevention or alleviation of allergic reactions in a subject
CC e.g. hay fever, rhinoconductivitis, rhinitis, asthma or systemic
CC anaphylaxis. The present sequence represents a recombinant allergen of
CC the invention. Note: The present sequence was not shown in the
CC specification but was created by the indexer using information in the
CC specification and the corresponding wild-type sequence
XX
SQ Sequence 129 AA;

Query Match 98.8%; Score 684; DB 5; Length 129;
Best Local Similarity 98.4%; Pred. No. 1.2e-72;
Matches 127; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LEVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120

Qy        121 IATHAKIRD 129
              |||||||:|
Db        121 IATHAKIQD 129
```

RESULT 3
ABG67016
ID ABG67016 standard; protein; 129 AA.
XX
AC ABG67016;
XX
DT 24-SEP-2002 (first entry)
XX
DE House dust mite allergen Der p 2 ALK-G mutant #6.
XX
KW Immunoglobulin E; IgE; allergen; allergy; mutein; hay fever;
KW rhinoconductivitis; rhinitis; asthma; systemic anaphylaxis; mutant;
KW vaccine; antiallergic; B cell epitope.
XX
OS Dermatophagoides pteronyssinus.
OS Synthetic.
XX
PN WO200240676-A2.
XX
PD 23-MAY-2002.
XX
PF 16-NOV-2001; 2001WO-DK000764.
XX
PR 16-NOV-2000; 2000DK-00001718.
PR 16-NOV-2000; 2000US-0249361P.
PR 14-JUN-2001; 2001US-0298170P.
XX
PA (ALKA-) ALK-ABELLO AS.
XX
PI Holm J, Ipsen H, Nedergaard Larsen J, Spangfort MD;
XX
DR WPI; 2002-508328/54.
DR N-PSDB; ABK95632.
XX
PT New recombinant mutant allergen, useful for preventing and/or treating
PT allergy, comprises multiple mutations and reduced immunoglobulin E
PT binding affinity.
XX
PS Example 6; Page; 210pp; English.
XX
CC The invention relates to a recombinant allergen (I) which is a mutant of
CC a naturally occurring allergen, where the mutant allergen has at least
CC four primary mutations, which each reduce the specific immunoglobulin E
CC (IgE) binding capability of the mutated allergen as compared to the IgE
CC binding capability of the naturally occurring allergen, where each
CC primary mutation is a substitution of one surface-exposed amino acid
CC residue with another residue, which does not occur in the same position
CC in the amino acid sequence of any known homologous protein within the
CC taxonomic species from which the naturally occurring allergen originates,
CC and each primary mutation is spaced from each other primary mutation by
CC at least 15 Angstrom , and the primary mutations are placed in such a
CC manner that at least one circular surface region with a area of 800
CC Angstrom ^2 comprises no mutation. Also included are a composition
CC comprising two or more of the recombinant allergens, where the variant
CC allergen is defined by having at least one primary mutation, which is
CC absent in at least one of the other variants, and for each variant no
CC secondary mutation is present within a radius of 15 Angstrom from each
CC absent primary mutation; a DNA sequence encoding the recombinant allergen
CC or its derivative, partial sequence or degenerated sequence, or a
CC sequence which hybridises to it under stringent conditions, where the
CC derivative, partial sequence, degenerated sequence or hybridising
CC sequence encodes a peptide having at least one B cell epitope; an
CC expression vector comprising the DNA and a host cell comprising the
CC vector. The recombinant allergen is useful as a pharmaceutical, for
CC preparing a pharmaceutical for preventing and/or treating allergy, or in
CC a diagnostic assay for assessing relevance, safety or outcome of therapy
CC of a subject, where an IgE containing sample of the subject is mixed with
CC the recombinant allergen and assessed for the level of reactivity between
CC the IgE in the sample and the recombinant allergen. The recombinant
CC allergen or compositions are useful for generating an immune response in
CC a subject, for vaccination or treatment of a subject or for the
CC treatment, prevention or alleviation of allergic reactions in a subject
CC e.g. hay fever, rhinoconductivitis, rhinitis, asthma or systemic
CC anaphylaxis. The present sequence represents a recombinant allergen of
CC the invention. Note: The present sequence was not shown in the
CC specification but was created by the indexer using information in the
CC specification and the corresponding wild-type sequence
XX
SQ Sequence 129 AA;

Query Match 98.8%; Score 684; DB 5; Length 129;
Best Local Similarity 98.4%; Pred. No. 1.2e-72;
Matches 127; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DQVDVKDCANHEIKKVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120

Qy        121 IATHAKIRD 129
              |||||||:|
Db        121 IATHAKIQD 129
```

RESULT 4
ABG67015
ID ABG67015 standard; protein; 129 AA.
XX
AC ABG67015;
XX
DT 24-SEP-2002 (first entry)
XX
DE House dust mite allergen Der p 2 ALK-G mutant #5.
XX
KW Immunoglobulin E; IgE; allergen; allergy; mutein; hay fever;
KW rhinoconductivitis; rhinitis; asthma; systemic anaphylaxis; mutant;
KW vaccine; antiallergic; B cell epitope.
XX
OS Dermatophagoides pteronyssinus.
OS Synthetic.
XX
PN WO200240676-A2.
XX
PD 23-MAY-2002.
XX
PF 16-NOV-2001; 2001WO-DK000764.
XX
PR 16-NOV-2000; 2000DK-00001718.
PR 16-NOV-2000; 2000US-0249361P.
PR 14-JUN-2001; 2001US-0298170P.
XX
PA (ALKA-) ALK-ABELLO AS.
XX
PI Holm J, Ipsen H, Nedergaard Larsen J, Spangfort MD;
XX
DR WPI; 2002-508328/54.
DR N-PSDB; ABK95631.
XX
PT New recombinant mutant allergen, useful for preventing and/or treating
PT allergy, comprises multiple mutations and reduced immunoglobulin E
PT binding affinity.
XX
PS Example 6; Page; 210pp; English.
XX
CC The invention relates to a recombinant allergen (I) which is a mutant of
CC a naturally occurring allergen, where the mutant allergen has at least
CC four primary mutations, which each reduce the specific immunoglobulin E
CC (IgE) binding capability of the mutated allergen as compared to the IgE
CC binding capability of the naturally occurring allergen, where each
CC primary mutation is a substitution of one surface-exposed amino acid
CC residue with another residue, which does not occur in the same position
CC in the amino acid sequence of any known homologous protein within the
CC taxonomic species from which the naturally occurring allergen originates,

CC and each primary mutation is spaced from each other primary mutation by
CC at least 15 Angstrom , and the primary mutations are placed in such a
CC manner that at least one circular surface region with a area of 800
CC Angstrom ^2 comprises no mutation. Also included are a composition
CC comprising two or more of the recombinant allergens, where the variant
CC allergen is defined by having at least one primary mutation, which is
CC absent in at least one of the other variants, and for each variant no
CC secondary mutation is present within a radius of 15 Angstrom from each
CC absent primary mutation; a DNA sequence encoding the recombinant allergen
CC or its derivative, partial sequence or degenerated sequence, or a
CC sequence which hybridises to it under stringent conditions, where the
CC derivative, partial sequence, degenerated sequence or hybridising
CC sequence encodes a peptide having at least one B cell epitope; an
CC expression vector comprising the DNA and a host cell comprising the
CC vector. The recombinant allergen is useful as a pharmaceutical, for
CC preparing a pharmaceutical for preventing and/or treating allergy, or in
CC a diagnostic assay for assessing relevance, safety or outcome of therapy
CC of a subject, where an IgE containing sample of the subject is mixed with
CC the recombinant allergen and assessed for the level of reactivity between
CC the IgE in the sample and the recombinant allergen. The recombinant
CC allergen or compositions are useful for generating an immune response in
CC a subject, for vaccination or treatment of a subject or for the
CC treatment, prevention or alleviation of allergic reactions in a subject
CC e.g. hay fever, rhinoconductivitis, rhinitis, asthma or systemic
CC anaphylaxis. The present sequence represents a recombinant allergen of
CC the invention. Note: The present sequence was not shown in the
CC specification but was created by the indexer using information in the
CC specification and the corresponding wild-type sequence
XX
SQ Sequence 129 AA;

Query Match 98.7%; Score 683; DB 5; Length 129;
Best Local Similarity 98.4%; Pred. No. 1.6e-72;
Matches 127; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              |||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||
Db          1 DQVDVKDCANHEIKEVLVPGCHGSEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120

Qy        121 IATHAKIRD 129
              |||||||:|
Db        121 IATHAKIQD 129
```

RESULT 5
ABG67014
ID ABG67014 standard; protein; 129 AA.
XX
AC ABG67014;
XX
DT 24-SEP-2002 (first entry)
XX
DE House dust mite allergen Der p 2 ALK-G mutant #4.
XX
KW Immunoglobulin E; IgE; allergen; allergy; mutein; hay fever;
KW rhinoconductivitis; rhinitis; asthma; systemic anaphylaxis; mutant;
KW vaccine; antiallergic; B cell epitope.
XX
OS Dermatophagoides pteronyssinus.
OS Synthetic.
XX
PN WO200240676-A2.
XX
PD 23-MAY-2002.
XX
PF 16-NOV-2001; 2001WO-DK000764.
XX
PR 16-NOV-2000; 2000DK-00001718.
PR 16-NOV-2000; 2000US-0249361P.
PR 14-JUN-2001; 2001US-0298170P.
XX
PA (ALKA-) ALK-ABELLO AS.
XX
PI Holm J, Ipsen H, Nedergaard Larsen J, Spangfort MD;
XX
DR WPI; 2002-508328/54.
DR N-PSDB; ABK95630.
XX
PT New recombinant mutant allergen, useful for preventing and/or treating
PT allergy, comprises multiple mutations and reduced immunoglobulin E
PT binding affinity.
XX
PS Example 6; Page; 210pp; English.
XX
CC The invention relates to a recombinant allergen (I) which is a mutant of
CC a naturally occurring allergen, where the mutant allergen has at least
CC four primary mutations, which each reduce the specific immunoglobulin E
CC (IgE) binding capability of the mutated allergen as compared to the IgE
CC binding capability of the naturally occurring allergen, where each
CC primary mutation is a substitution of one surface-exposed amino acid
CC residue with another residue, which does not occur in the same position
CC in the amino acid sequence of any known homologous protein within the
CC taxonomic species from which the naturally occurring allergen originates,
CC and each primary mutation is spaced from each other primary mutation by
CC at least 15 Angstrom , and the primary mutations are placed in such a
CC manner that at least one circular surface region with a area of 800
CC Angstrom ^2 comprises no mutation. Also included are a composition
CC comprising two or more of the recombinant allergens, where the variant
CC allergen is defined by having at least one primary mutation, which is
CC absent in at least one of the other variants, and for each variant no
CC secondary mutation is present within a radius of 15 Angstrom from each
CC absent primary mutation; a DNA sequence encoding the recombinant allergen
CC or its derivative, partial sequence or degenerated sequence, or a
CC sequence which hybridises to it under stringent conditions, where the
CC derivative, partial sequence, degenerated sequence or hybridising
CC sequence encodes a peptide having at least one B cell epitope; an
CC expression vector comprising the DNA and a host cell comprising the
CC vector. The recombinant allergen is useful as a pharmaceutical, for
CC preparing a pharmaceutical for preventing and/or treating allergy, or in
CC a diagnostic assay for assessing relevance, safety or outcome of therapy
CC of a subject, where an IgE containing sample of the subject is mixed with
CC the recombinant allergen and assessed for the level of reactivity between
CC the IgE in the sample and the recombinant allergen. The recombinant
CC allergen or compositions are useful for generating an immune response in
CC a subject, for vaccination or treatment of a subject or for the
CC treatment, prevention or alleviation of allergic reactions in a subject
CC e.g. hay fever, rhinoconductivitis, rhinitis, asthma or systemic
CC anaphylaxis. The present sequence represents a recombinant allergen of
CC the invention. Note: The present sequence was not shown in the
CC specification but was created by the indexer using information in the
CC specification and the corresponding wild-type sequence
XX
SQ Sequence 129 AA;

Query Match 98.7%; Score 683; DB 5; Length 129;
Best Local Similarity 98.4%; Pred. No. 1.6e-72;
Matches 127; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSKTAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120

Qy        121 IATHAKIRD 129
              |||||||:|
Db        121 IATHAKIQD 129
```

RESULT 6

```
ABG67012
ID   ABG67012 standard; protein; 129 AA.
XX
AC   ABG67012;
XX
DT   24-SEP-2002  (first entry)
XX
DE   House dust mite allergen Der p 2 ALK-G mutant #2.
XX
KW   Immunoglobulin E; IgE; allergen; allergy; mutein; hay fever;
KW   rhinoconductivitis; rhinitis; asthma; systemic anaphylaxis; mutant;
KW   vaccine; antiallergic; B cell epitope.
XX
OS   Dermatophagoides pteronyssinus.
OS   Synthetic.
XX
PN   WO200240676-A2.
XX
PD   23-MAY-2002.
XX
PF   16-NOV-2001; 2001WO-DK000764.
XX
PR   16-NOV-2000; 2000DK-00001718.
PR   16-NOV-2000; 2000US-0249361P.
PR   14-JUN-2001; 2001US-0298170P.
XX
PA   (ALKA-) ALK-ABELLO AS.
XX
PI   Holm J,  Ipsen H,  Nedergaard Larsen J,  Spangfort MD;
XX
DR   WPI; 2002-508328/54.
DR   N-PSDB; ABK95628.
XX
PT   New recombinant mutant allergen, useful for preventing and/or treating
PT   allergy, comprises multiple mutations and reduced immunoglobulin E
PT   binding affinity.
XX
PS   Example 6; Page; 210pp; English.
XX
CC   The invention relates to a recombinant allergen (I) which is a mutant of
CC   a naturally occurring allergen, where the mutant allergen has at least
CC   four primary mutations, which each reduce the specific immunoglobulin E
CC   (IgE) binding capability of the mutated allergen as compared to the IgE
CC   binding capability of the naturally occurring allergen, where each
CC   primary mutation is a substitution of one surface-exposed amino acid
CC   residue with another residue, which does not occur in the same position
CC   in the amino acid sequence of any known homologous protein within the
CC   taxonomic species from which the naturally occurring allergen originates,
CC   and each primary mutation is spaced from each other primary mutation by
CC   at least 15 Angstrom , and the primary mutations are placed in such a
CC   manner that at least one circular surface region with a area of 800
CC   Angstrom ^2 comprises no mutation. Also included are a composition
CC   comprising two or more of the recombinant allergens, where the variant
CC   allergen is defined by having at least one primary mutation, which is
CC   absent in at least one of the other variants, and for each variant no
CC   secondary mutation is present within a radius of 15 Angstrom from each
CC   absent primary mutation; a DNA sequence encoding the recombinant allergen
CC   or its derivative, partial sequence or degenerated sequence, or a
CC   sequence which hybridises to it under stringent conditions, where the
CC   derivative, partial sequence, degenerated sequence or hybridising
CC   sequence encodes a peptide having at least one B cell epitope; an
CC   expression vector comprising the DNA and a host cell comprising the
CC   vector. The recombinant allergen is useful as a pharmaceutical, for
CC   preparing a pharmaceutical for preventing and/or treating allergy, or in
CC   a diagnostic assay for assessing relevance, safety or outcome of therapy
CC   of a subject, where an IgE containing sample of the subject is mixed with
CC   the recombinant allergen and assessed for the level of reactivity between
CC   the IgE in the sample and the recombinant allergen. The recombinant
CC   allergen or compositions are useful for generating an immune response in
CC   a subject, for vaccination or treatment of a subject or for the
CC   treatment, prevention or alleviation of allergic reactions in a subject
CC   e.g. hay fever, rhinoconductivitis, rhinitis, asthma or systemic
CC   anaphylaxis. The present sequence represents a recombinant allergen of
CC   the invention. Note: The present sequence was not shown in the
CC   specification but was created by the indexer using information in the
CC   specification and the corresponding wild-type sequence
XX
SQ   Sequence 129 AA;

  Query Match             98.6%;  Score 682;  DB 5;  Length 129;
  Best Local Similarity   98.4%;  Pred. No. 2.1e-72;
  Matches  127;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPKSENVVVTVKVLGDNGVLACA 120

Qy        121 IATHAKIRD 129
              |||||||:|
Db        121 IATHAKIQD 129


RESULT 7
ABG67019
ID   ABG67019 standard; protein; 129 AA.
XX
AC   ABG67019;
XX
DT   24-SEP-2002  (first entry)
XX
DE   House dust mite allergen Der p 2 ALK-G mutant #9.
XX
KW   Immunoglobulin E; IgE; allergen; allergy; mutein; hay fever;
KW   rhinoconductivitis; rhinitis; asthma; systemic anaphylaxis; mutant;
KW   vaccine; antiallergic; B cell epitope.
XX
OS   Dermatophagoides pteronyssinus.
OS   Synthetic.
XX
PN   WO200240676-A2.
XX
PD   23-MAY-2002.
XX
PF   16-NOV-2001; 2001WO-DK000764.
XX
PR   16-NOV-2000; 2000DK-00001718.
PR   16-NOV-2000; 2000US-0249361P.
PR   14-JUN-2001; 2001US-0298170P.
XX
PA   (ALKA-) ALK-ABELLO AS.
XX
PI   Holm J,  Ipsen H,  Nedergaard Larsen J,  Spangfort MD;
XX
DR   WPI; 2002-508328/54.
DR   N-PSDB; ABK95635.
XX
PT   New recombinant mutant allergen, useful for preventing and/or treating
PT   allergy, comprises multiple mutations and reduced immunoglobulin E
PT   binding affinity.
XX
PS   Example 6; Page; 210pp; English.
XX
CC   The invention relates to a recombinant allergen (I) which is a mutant of
CC   a naturally occurring allergen, where the mutant allergen has at least
CC   four primary mutations, which each reduce the specific immunoglobulin E
CC   (IgE) binding capability of the mutated allergen as compared to the IgE
CC   binding capability of the naturally occurring allergen, where each
CC   primary mutation is a substitution of one surface-exposed amino acid
CC   residue with another residue, which does not occur in the same position
CC   in the amino acid sequence of any known homologous protein within the
CC   taxonomic species from which the naturally occurring allergen originates,
CC   and each primary mutation is spaced from each other primary mutation by
```

CC at least 15 Angstrom , and the primary mutations are placed in such a
CC manner that at least one circular surface region with a area of 800
CC Angstrom ^2 comprises no mutation. Also included are a composition
CC comprising two or more of the recombinant allergens, where the variant
CC allergen is defined by having at least one primary mutation, which is
CC absent in at least one of the other variants, and for each variant no
CC secondary mutation is present within a radius of 15 Angstrom from each
CC absent primary mutation; a DNA sequence encoding the recombinant allergen
CC or its derivative, partial sequence or degenerated sequence, or a
CC sequence which hybridises to it under stringent conditions, where the
CC derivative, partial sequence, degenerated sequence or hybridising
CC sequence encodes a peptide having at least one B cell epitope; an
CC expression vector comprising the DNA and a host cell comprising the
CC vector. The recombinant allergen is useful as a pharmaceutical, for
CC preparing a pharmaceutical for preventing and/or treating allergy, or in
CC a diagnostic assay for assessing relevance, safety or outcome of therapy
CC of a subject, where an IgE containing sample of the subject is mixed with
CC the recombinant allergen and assessed for the level of reactivity between
CC the IgE in the sample and the recombinant allergen. The recombinant
CC allergen or compositions are useful for generating an immune response in
CC a subject, for vaccination or treatment of a subject or for the
CC treatment, prevention or alleviation of allergic reactions in a subject
CC e.g. hay fever, rhinoconductivitis, rhinitis, asthma or systemic
CC anaphylaxis. The present sequence represents a recombinant allergen of
CC the invention. Note: The present sequence was not shown in the
CC specification but was created by the indexer using information in the
CC specification and the corresponding wild-type sequence
XX
SQ Sequence 129 AA;

Query Match 94.9%; Score 657; DB 5; Length 129;
Best Local Similarity 95.3%; Pred. No. 1.9e-69;
Matches 123; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIHSGKPFQLEALFEANQNSATAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | |||||||||||:|| ||||||||||||||||||||||||||||||||||||||||||||
Db         61 LEVDVPGIDPNACNYMKCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120

Qy        121 IATHAKIRD 129
                |||||||:|
Db        121 IATHAKIQD 129
```

RESULT 8
ABG67022
ID ABG67022 standard; protein; 129 AA.
XX
AC ABG67022;
XX
DT 24-SEP-2002 (first entry)
XX
DE House dust mite allergen Der p 2 ALK-G mutant #12.
XX
KW Immunoglobulin E; IgE; allergen; allergy; mutein; hay fever;
KW rhinoconductivitis; rhinitis; asthma; systemic anaphylaxis; mutant;
KW vaccine; antiallergic; B cell epitope.
XX
OS Dermatophagoides pteronyssinus.
OS Synthetic.
XX
PN WO200240676-A2.
XX
PD 23-MAY-2002.
XX
PF 16-NOV-2001; 2001WO-DK000764.
XX
PR 16-NOV-2000; 2000DK-00001718.
PR 16-NOV-2000; 2000US-0249361P.
PR 14-JUN-2001; 2001US-0298170P.
XX
PA (ALKA-) ALK-ABELLO AS.
XX
PI Holm J, Ipsen H, Nedergaard Larsen J, Spangfort MD;
XX
DR WPI; 2002-508328/54.
DR N-PSDB; ABK95638.
XX
PT New recombinant mutant allergen, useful for preventing and/or treating
PT allergy, comprises multiple mutations and reduced immunoglobulin E
PT binding affinity.
XX
PS Example 6; Page; 210pp; English.
XX
CC The invention relates to a recombinant allergen (I) which is a mutant of
CC a naturally occurring allergen, where the mutant allergen has at least
CC four primary mutations, which each reduce the specific immunoglobulin E
CC (IgE) binding capability of the mutated allergen as compared to the IgE
CC binding capability of the naturally occurring allergen, where each
CC primary mutation is a substitution of one surface-exposed amino acid
CC residue with another residue, which does not occur in the same position
CC in the amino acid sequence of any known homologous protein within the
CC taxonomic species from which the naturally occurring allergen originates,
CC and each primary mutation is spaced from each other primary mutation by
CC at least 15 Angstrom , and the primary mutations are placed in such a
CC manner that at least one circular surface region with a area of 800
CC Angstrom ^2 comprises no mutation. Also included are a composition
CC comprising two or more of the recombinant allergens, where the variant
CC allergen is defined by having at least one primary mutation, which is
CC absent in at least one of the other variants, and for each variant no
CC secondary mutation is present within a radius of 15 Angstrom from each
CC absent primary mutation; a DNA sequence encoding the recombinant allergen
CC or its derivative, partial sequence or degenerated sequence, or a
CC sequence which hybridises to it under stringent conditions, where the
CC derivative, partial sequence, degenerated sequence or hybridising
CC sequence encodes a peptide having at least one B cell epitope; an
CC expression vector comprising the DNA and a host cell comprising the
CC vector. The recombinant allergen is useful as a pharmaceutical, for
CC preparing a pharmaceutical for preventing and/or treating allergy, or in
CC a diagnostic assay for assessing relevance, safety or outcome of therapy
CC of a subject, where an IgE containing sample of the subject is mixed with
CC the recombinant allergen and assessed for the level of reactivity between
CC the IgE in the sample and the recombinant allergen. The recombinant
CC allergen or compositions are useful for generating an immune response in
CC a subject, for vaccination or treatment of a subject or for the
CC treatment, prevention or alleviation of allergic reactions in a subject
CC e.g. hay fever, rhinoconductivitis, rhinitis, asthma or systemic
CC anaphylaxis. The present sequence represents a recombinant allergen of
CC the invention. Note: The present sequence was not shown in the
CC specification but was created by the indexer using information in the
CC specification and the corresponding wild-type sequence
XX
SQ Sequence 129 AA;

Query Match 94.9%; Score 657; DB 5; Length 129;
Best Local Similarity 95.3%; Pred. No. 1.9e-69;
Matches 123; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              |||||||||||||:|||||||||||||  ||||||||||||||||||||||||||||||
Db          1 DQVDVKDCANHEIKKVLVPGCHGNEPCIIHSGKPFQLEALFEANQNSATAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              |||||||||||||:|| ||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSVDVPGIDPNACNYMKCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120

Qy        121 IATHAKIRD 129
                |||||||:|
Db        121 IATHAKIQD 129
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RESULT 9
ABG67021

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ID   ABG67021 standard; protein; 129 AA.
XX
AC   ABG67021;
XX
DT   24-SEP-2002  (first entry)
XX
DE   House dust mite allergen Der p 2 ALK-G mutant #11.
XX
KW   Immunoglobulin E; IgE; allergen; allergy; mutein; hay fever;
KW   rhinoconductivitis; rhinitis; asthma; systemic anaphylaxis; mutant;
KW   vaccine; antiallergic; B cell epitope.
XX
OS   Dermatophagoides pteronyssinus.
OS   Synthetic.
XX
PN   WO200240676-A2.
XX
PD   23-MAY-2002.
XX
PF   16-NOV-2001; 2001WO-DK000764.
XX
PR   16-NOV-2000; 2000DK-00001718.
PR   16-NOV-2000; 2000US-0249361P.
PR   14-JUN-2001; 2001US-0298170P.
XX
PA   (ALKA-) ALK-ABELLO AS.
XX
PI   Holm J,  Ipsen H,  Nedergaard Larsen J,  Spangfort MD;
XX
DR   WPI; 2002-508328/54.
DR   N-PSDB; ABK95637.
XX
PT   New recombinant mutant allergen, useful for preventing and/or treating
PT   allergy, comprises multiple mutations and reduced immunoglobulin E
PT   binding affinity.
XX
PS   Example 6; Page; 210pp; English.
XX
CC   The invention relates to a recombinant allergen (I) which is a mutant of
CC   a naturally occurring allergen, where the mutant allergen has at least
CC   four primary mutations, which each reduce the specific immunoglobulin E
CC   (IgE) binding capability of the mutated allergen as compared to the IgE
CC   binding capability of the naturally occurring allergen, where each
CC   primary mutation is a substitution of one surface-exposed amino acid
CC   residue with another residue, which does not occur in the same position
CC   in the amino acid sequence of any known homologous protein within the
CC   taxonomic species from which the naturally occurring allergen originates,
CC   and each primary mutation is spaced from each other primary mutation by
CC   at least 15 Angstrom , and the primary mutations are placed in such a
CC   manner that at least one circular surface region with a area of 800
CC   Angstrom ^2 comprises no mutation. Also included are a composition
CC   comprising two or more of the recombinant allergens, where the variant
CC   allergen is defined by having at least one primary mutation, which is
CC   absent in at least one of the other variants, and for each variant no
CC   secondary mutation is present within a radius of 15 Angstrom from each
CC   absent primary mutation; a DNA sequence encoding the recombinant allergen
CC   or its derivative, partial sequence or degenerated sequence, or a
CC   sequence which hybridises to it under stringent conditions, where the
CC   derivative, partial sequence, degenerated sequence or hybridising
CC   sequence encodes a peptide having at least one B cell epitope; an
CC   expression vector comprising the DNA and a host cell comprising the
CC   vector. The recombinant allergen is useful as a pharmaceutical, for
CC   preparing a pharmaceutical for preventing and/or treating allergy, or in
CC   a diagnostic assay for assessing relevance, safety or outcome of therapy
CC   of a subject, where an IgE containing sample of the subject is mixed with
CC   the recombinant allergen and assessed for the level of reactivity between
CC   the IgE in the sample and the recombinant allergen. The recombinant
CC   allergen or compositions are useful for generating an immune response in
CC   a subject, for vaccination or treatment of a subject or for the
CC   treatment, prevention or alleviation of allergic reactions in a subject
CC   e.g. hay fever, rhinoconductivitis, rhinitis, asthma or systemic
CC   anaphylaxis. The present sequence represents a recombinant allergen of
CC   the invention. Note: The present sequence was not shown in the
CC   specification but was created by the indexer using information in the
CC   specification and the corresponding wild-type sequence
XX
SQ   Sequence 129 AA;

  Query Match             94.8%;  Score 656;  DB 5;  Length 129;
  Best Local Similarity   95.3%;  Pred. No. 2.5e-69;
  Matches  123;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||||||||||||:|||||  ||||||||||||||||||||||||||||||
Db          1 DQVDVKDCANHEIKEVLVPGCHGSEPCIIHSGKPFQLEALFEANQNSATAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              |||||||||||||:|| ||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSVDVPGIDPNACNYMKCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120

Qy        121 IATHAKIRD 129
              |||||||:|
Db        121 IATHAKIQD 129


RESULT 10
ABG67020
ID   ABG67020 standard; protein; 129 AA.
XX
AC   ABG67020;
XX
DT   24-SEP-2002  (first entry)
XX
DE   House dust mite allergen Der p 2 ALK-G mutant #10.
XX
KW   Immunoglobulin E; IgE; allergen; allergy; mutein; hay fever;
KW   rhinoconductivitis; rhinitis; asthma; systemic anaphylaxis; mutant;
KW   vaccine; antiallergic; B cell epitope.
XX
OS   Dermatophagoides pteronyssinus.
OS   Synthetic.
XX
PN   WO200240676-A2.
XX
PD   23-MAY-2002.
XX
PF   16-NOV-2001; 2001WO-DK000764.
XX
PR   16-NOV-2000; 2000DK-00001718.
PR   16-NOV-2000; 2000US-0249361P.
PR   14-JUN-2001; 2001US-0298170P.
XX
PA   (ALKA-) ALK-ABELLO AS.
XX
PI   Holm J,  Ipsen H,  Nedergaard Larsen J,  Spangfort MD;
XX
DR   WPI; 2002-508328/54.
DR   N-PSDB; ABK95636.
XX
PT   New recombinant mutant allergen, useful for preventing and/or treating
PT   allergy, comprises multiple mutations and reduced immunoglobulin E
PT   binding affinity.
XX
PS   Example 6; Page; 210pp; English.
XX
CC   The invention relates to a recombinant allergen (I) which is a mutant of
CC   a naturally occurring allergen, where the mutant allergen has at least
CC   four primary mutations, which each reduce the specific immunoglobulin E
CC   (IgE) binding capability of the mutated allergen as compared to the IgE
CC   binding capability of the naturally occurring allergen, where each
CC   primary mutation is a substitution of one surface-exposed amino acid
CC   residue with another residue, which does not occur in the same position
CC   in the amino acid sequence of any known homologous protein within the
CC   taxonomic species from which the naturally occurring allergen originates,
CC   and each primary mutation is spaced from each other primary mutation by
CC   at least 15 Angstrom , and the primary mutations are placed in such a
```

```
CC   manner that at least one circular surface region with a area of 800
CC   Angstrom ^2 comprises no mutation. Also included are a composition
CC   comprising two or more of the recombinant allergens, where the variant
CC   allergen is defined by having at least one primary mutation, which is
CC   absent in at least one of the other variants, and for each variant no
CC   secondary mutation is present within a radius of 15 Angstrom from each
CC   absent primary mutation; a DNA sequence encoding the recombinant allergen
CC   or its derivative, partial sequence or degenerated sequence, or a
CC   sequence which hybridises to it under stringent conditions, where the
CC   derivative, partial sequence, degenerated sequence or hybridising
CC   sequence encodes a peptide having at least one B cell epitope; an
CC   expression vector comprising the DNA and a host cell comprising the
CC   vector. The recombinant allergen is useful as a pharmaceutical, for
CC   preparing a pharmaceutical for preventing and/or treating allergy, or in
CC   a diagnostic assay for assessing relevance, safety or outcome of therapy
CC   of a subject, where an IgE containing sample of the subject is mixed with
CC   the recombinant allergen and assessed for the level of reactivity between
CC   the IgE in the sample and the recombinant allergen. The recombinant
CC   allergen or compositions are useful for generating an immune response in
CC   a subject, for vaccination or treatment of a subject or for the
CC   treatment, prevention or alleviation of allergic reactions in a subject
CC   e.g. hay fever, rhinoconductivitis, rhinitis, asthma or systemic
CC   anaphylaxis. The present sequence represents a recombinant allergen of
CC   the invention. Note: The present sequence was not shown in the
CC   specification but was created by the indexer using information in the
CC   specification and the corresponding wild-type sequence
XX
SQ   Sequence 129 AA;

  Query Match             94.8%;  Score 656;  DB 5;  Length 129;
  Best Local Similarity   95.3%;  Pred. No. 2.5e-69;
  Matches  123;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||||||||||||||||  |||||||||||||||| ||||||||||||
Db          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIHSGKPFQLEALFEANQNSKTAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              |||||||||||||:|| ||||||||||||||||||||||||||||||||||||||||||
Db         61 LSVDVPGIDPNACNYMKCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120

Qy        121 IATHAKIRD 129
              |||||||:|
Db        121 IATHAKIQD 129


RESULT 11
ABG67018
ID   ABG67018 standard; protein; 129 AA.
XX
AC   ABG67018;
XX
DT   24-SEP-2002  (first entry)
XX
DE   House dust mite allergen Der p 2 ALK-G mutant #8.
XX
KW   Immunoglobulin E; IgE; allergen; allergy; mutein; hay fever;
KW   rhinoconductivitis; rhinitis; asthma; systemic anaphylaxis; mutant;
KW   vaccine; antiallergic; B cell epitope.
XX
OS   Dermatophagoides pteronyssinus.
OS   Synthetic.
XX
PN   WO200240676-A2.
XX
PD   23-MAY-2002.
XX
PF   16-NOV-2001; 2001WO-DK000764.
XX
PR   16-NOV-2000; 2000DK-00001718.
PR   16-NOV-2000; 2000US-0249361P.
PR   14-JUN-2001; 2001US-0298170P.
XX
PA   (ALKA-) ALK-ABELLO AS.
XX
PI   Holm J,  Ipsen H,  Nedergaard Larsen J,  Spangfort MD;
XX
DR   WPI; 2002-508328/54.
DR   N-PSDB; ABK95634.
XX
PT   New recombinant mutant allergen, useful for preventing and/or treating
PT   allergy, comprises multiple mutations and reduced immunoglobulin E
PT   binding affinity.
XX
PS   Example 6; Page; 210pp; English.
XX
CC   The invention relates to a recombinant allergen (I) which is a mutant of
CC   a naturally occurring allergen, where the mutant allergen has at least
CC   four primary mutations, which each reduce the specific immunoglobulin E
CC   (IgE) binding capability of the mutated allergen as compared to the IgE
CC   binding capability of the naturally occurring allergen, where each
CC   primary mutation is a substitution of one surface-exposed amino acid
CC   residue with another residue, which does not occur in the same position
CC   in the amino acid sequence of any known homologous protein within the
CC   taxonomic species from which the naturally occurring allergen originates,
CC   and each primary mutation is spaced from each other primary mutation by
CC   at least 15 Angstrom , and the primary mutations are placed in such a
CC   manner that at least one circular surface region with a area of 800
CC   Angstrom ^2 comprises no mutation. Also included are a composition
CC   comprising two or more of the recombinant allergens, where the variant
CC   allergen is defined by having at least one primary mutation, which is
CC   absent in at least one of the other variants, and for each variant no
CC   secondary mutation is present within a radius of 15 Angstrom from each
CC   absent primary mutation; a DNA sequence encoding the recombinant allergen
CC   or its derivative, partial sequence or degenerated sequence, or a
CC   sequence which hybridises to it under stringent conditions, where the
CC   derivative, partial sequence, degenerated sequence or hybridising
CC   sequence encodes a peptide having at least one B cell epitope; an
CC   expression vector comprising the DNA and a host cell comprising the
CC   vector. The recombinant allergen is useful as a pharmaceutical, for
CC   preparing a pharmaceutical for preventing and/or treating allergy, or in
CC   a diagnostic assay for assessing relevance, safety or outcome of therapy
CC   of a subject, where an IgE containing sample of the subject is mixed with
CC   the recombinant allergen and assessed for the level of reactivity between
CC   the IgE in the sample and the recombinant allergen. The recombinant
CC   allergen or compositions are useful for generating an immune response in
CC   a subject, for vaccination or treatment of a subject or for the
CC   treatment, prevention or alleviation of allergic reactions in a subject
CC   e.g. hay fever, rhinoconductivitis, rhinitis, asthma or systemic
CC   anaphylaxis. The present sequence represents a recombinant allergen of
CC   the invention. Note: The present sequence was not shown in the
CC   specification but was created by the indexer using information in the
CC   specification and the corresponding wild-type sequence
XX
SQ   Sequence 129 AA;

  Query Match             94.7%;  Score 655;  DB 5;  Length 129;
  Best Local Similarity   95.3%;  Pred. No. 3.3e-69;
  Matches  123;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||||||||||||||||  |||||||||||||||||||||||||||||
Db          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIHSGKPFQLEALFEANQNSATAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              |||||||||||||:|| ||||||||||||||||||| ||||||||||||||||||||
Db         61 LSVDVPGIDPNACNYMKCPLVNGQQYDIKYTWNVPKIAPKSENVVVTVKVLGDNGVLACA 120

Qy        121 IATHAKIRD 129
              |||||||:|
Db        121 IATHAKIQD 129


RESULT 12
ABG67017
ID   ABG67017 standard; protein; 129 AA.
```

```
XX
AC   ABG67017;
XX
DT   24-SEP-2002  (first entry)
XX
DE   House dust mite allergen Der p 2 ALK-G mutant #7.
XX
KW   Immunoglobulin E; IgE; allergen; allergy; mutein; hay fever;
KW   rhinoconductivitis; rhinitis; asthma; systemic anaphylaxis; mutant;
KW   vaccine; antiallergic; B cell epitope.
XX
OS   Dermatophagoides pteronyssinus.
OS   Synthetic.
XX
PN   WO200240676-A2.
XX
PD   23-MAY-2002.
XX
PF   16-NOV-2001; 2001WO-DK000764.
XX
PR   16-NOV-2000; 2000DK-00001718.
PR   16-NOV-2000; 2000US-0249361P.
PR   14-JUN-2001; 2001US-0298170P.
XX
PA   (ALKA-) ALK-ABELLO AS.
XX
PI   Holm J,  Ipsen H,  Nedergaard Larsen J,  Spangfort MD;
XX
DR   WPI; 2002-508328/54.
DR   N-PSDB; ABK95633.
XX
PT   New recombinant mutant allergen, useful for preventing and/or treating
PT   allergy, comprises multiple mutations and reduced immunoglobulin E
PT   binding affinity.
XX
PS   Example 6; Page; 210pp; English.
XX
CC   The invention relates to a recombinant allergen (I) which is a mutant of
CC   a naturally occurring allergen, where the mutant allergen has at least
CC   four primary mutations, which each reduce the specific immunoglobulin E
CC   (IgE) binding capability of the mutated allergen as compared to the IgE
CC   binding capability of the naturally occurring allergen, where each
CC   primary mutation is a substitution of one surface-exposed amino acid
CC   residue with another residue, which does not occur in the same position
CC   in the amino acid sequence of any known homologous protein within the
CC   taxonomic species from which the naturally occurring allergen originates,
CC   and each primary mutation is spaced from each other primary mutation by
CC   at least 15 Angstrom , and the primary mutations are placed in such a
CC   manner that at least one circular surface region with a area of 800
CC   Angstrom ^2 comprises no mutation. Also included are a composition
CC   comprising two or more of the recombinant allergens, where the variant
CC   allergen is defined by having at least one primary mutation, which is
CC   absent in at least one of the other variants, and for each variant no
CC   secondary mutation is present within a radius of 15 Angstrom from each
CC   absent primary mutation; a DNA sequence encoding the recombinant allergen
CC   or its derivative, partial sequence or degenerated sequence, or a
CC   sequence which hybridises to it under stringent conditions, where the
CC   derivative, partial sequence, degenerated sequence or hybridising
CC   sequence encodes a peptide having at least one B cell epitope; an
CC   expression vector comprising the DNA and a host cell comprising the
CC   vector. The recombinant allergen is useful as a pharmaceutical, for
CC   preparing a pharmaceutical for preventing and/or treating allergy, or in
CC   a diagnostic assay for assessing relevance, safety or outcome of therapy
CC   of a subject, where an IgE containing sample of the subject is mixed with
CC   the recombinant allergen and assessed for the level of reactivity between
CC   the IgE in the sample and the recombinant allergen. The recombinant
CC   allergen or compositions are useful for generating an immune response in
CC   a subject, for vaccination or treatment of a subject or for the
CC   treatment, prevention or alleviation of allergic reactions in a subject
CC   e.g. hay fever, rhinoconductivitis, rhinitis, asthma or systemic
CC   anaphylaxis. The present sequence represents a recombinant allergen of
CC   the invention. Note: The present sequence was not shown in the
CC   specification but was created by the indexer using information in the
CC   specification and the corresponding wild-type sequence
XX
SQ   Sequence 129 AA;

  Query Match             94.7%;  Score 655;  DB 5;  Length 129;
  Best Local Similarity   95.3%;  Pred. No. 3.3e-69;
  Matches  123;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIHSGKPFQLEALFEANQNSATAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              |||||||||||||:|| |||| ||||||||||||||||||||||||||||||||||||||
Db         61 LSVDVPGIDPNACNYMKCPLVKGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120

Qy        121 IATHAKIRD 129
              |||||||:|
Db        121 IATHAKIQD 129


RESULT 13
ABG67010
ID   ABG67010 standard; protein; 129 AA.
XX
AC   ABG67010;
XX
DT   24-SEP-2002  (first entry)
XX
DE   House dust mite allergen Der p 2 ALK-G.
XX
KW   Immunoglobulin E; IgE; allergen; allergy; hay fever; rhinoconductivitis;
KW   rhinitis; asthma; systemic anaphylaxis; vaccine; antiallergic;
KW   B cell epitope.
XX
OS   Dermatophagoides pteronyssinus.
XX
PN   WO200240676-A2.
XX
PD   23-MAY-2002.
XX
PF   16-NOV-2001; 2001WO-DK000764.
XX
PR   16-NOV-2000; 2000DK-00001718.
PR   16-NOV-2000; 2000US-0249361P.
PR   14-JUN-2001; 2001US-0298170P.
XX
PA   (ALKA-) ALK-ABELLO AS.
XX
PI   Holm J,  Ipsen H,  Nedergaard Larsen J,  Spangfort MD;
XX
DR   WPI; 2002-508328/54.
DR   N-PSDB; ABK95626.
XX
PT   New recombinant mutant allergen, useful for preventing and/or treating
PT   allergy, comprises multiple mutations and reduced immunoglobulin E
PT   binding affinity.
XX
PS   Example 6; Page 96; 210pp; English.
XX
CC   The invention relates to a recombinant allergen (I) which is a mutant of
CC   a naturally occurring allergen, where the mutant allergen has at least
CC   four primary mutations, which each reduce the specific immunoglobulin E
CC   (IgE) binding capability of the mutated allergen as compared to the IgE
CC   binding capability of the naturally occurring allergen, where each
CC   primary mutation is a substitution of one surface-exposed amino acid
CC   residue with another residue, which does not occur in the same position
CC   in the amino acid sequence of any known homologous protein within the
CC   taxonomic species from which the naturally occurring allergen originates,
CC   and each primary mutation is spaced from each other primary mutation by
CC   at least 15 Angstrom , and the primary mutations are placed in such a
CC   manner that at least one circular surface region with a area of 800
CC   Angstrom ^2 comprises no mutation. Also included are a composition
```

CC comprising two or more of the recombinant allergens, where the variant
CC allergen is defined by having at least one primary mutation, which is
CC absent in at least one of the other variants, and for each variant no
CC secondary mutation is present within a radius of 15 Angstrom from each
CC absent primary mutation; a DNA sequence encoding the recombinant allergen
CC or its derivative, partial sequence or degenerated sequence, or a
CC sequence which hybridises to it under stringent conditions, where the
CC derivative, partial sequence, degenerated sequence or hybridising
CC sequence encodes a peptide having at least one B cell epitope; an
CC expression vector comprising the DNA and a host cell comprising the
CC vector. The recombinant allergen is useful as a pharmaceutical, for
CC preparing a pharmaceutical for preventing and/or treating allergy, or in
CC a diagnostic assay for assessing relevance, safety or outcome of therapy
CC of a subject, where an IgE containing sample of the subject is mixed with
CC the recombinant allergen and assessed for the level of reactivity between
CC the IgE in the sample and the recombinant allergen. The recombinant
CC allergen or compositions are useful for generating an immune response in
CC a subject, for vaccination or treatment of a subject or for the
CC treatment, prevention or alleviation of allergic reactions in a subject
CC e.g. hay fever, rhinoconductivitis, rhinitis, asthma or systemic
CC anaphylaxis. The present sequence represents a wild-type allergen of the
CC invention
XX
SQ Sequence 129 AA;

Query Match 93.6%; Score 648; DB 5; Length 129;
Best Local Similarity 93.8%; Pred. No. 2.2e-68;
Matches 121; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||:||||||||:||||| |||||||||||||||| ||||||||||||
Db          1 DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEALFEANQNSKTAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | |||||||||||||| |||| |||||||||||||||| ||||||||||||||||||||
Db         61 LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVLGDNGVLACA 120

Qy        121 IATHAKIRD 129
              |||||||||
Db        121 IATHAKIRD 129
```

RESULT 14
ABG66996
ID ABG66996 standard; protein; 129 AA.
XX
AC ABG66996;
XX
DT 24-SEP-2002 (first entry)
XX
DE House dust mite allergen Der p 2 isoform ALK-120.
XX
KW Immunoglobulin E; IgE; allergen; allergy; hay fever; house dust mite;
KW rhinoconductivitis; rhinitis; asthma; systemic anaphylaxis; isoform;
KW vaccine; antiallergic; B cell epitope; Der p 2.
XX
OS Dermatophagoides pteronyssinus.
XX
PN WO200240676-A2.
XX
PD 23-MAY-2002.
XX
PF 16-NOV-2001; 2001WO-DK000764.
XX
PR 16-NOV-2000; 2000DK-00001718.
PR 16-NOV-2000; 2000US-0249361P.
PR 14-JUN-2001; 2001US-0298170P.
XX
PA (ALKA-) ALK-ABELLO AS.
XX
PI Holm J, Ipsen H, Nedergaard Larsen J, Spangfort MD;
XX
DR WPI; 2002-508328/54.
XX
PT New recombinant mutant allergen, useful for preventing and/or treating
PT allergy, comprises multiple mutations and reduced immunoglobulin E
PT binding affinity.
XX
PS Example 5; Page; 210pp; English.
XX
CC The invention relates to a recombinant allergen (I) which is a mutant of
CC a naturally occurring allergen, where the mutant allergen has at least
CC four primary mutations, which each reduce the specific immunoglobulin E
CC (IgE) binding capability of the mutated allergen as compared to the IgE
CC binding capability of the naturally occurring allergen, where each
CC primary mutation is a substitution of one surface-exposed amino acid
CC residue with another residue, which does not occur in the same position
CC in the amino acid sequence of any known homologous protein within the
CC taxonomic species from which the naturally occurring allergen originates,
CC and each primary mutation is spaced from each other primary mutation by
CC at least 15 Angstrom , and the primary mutations are placed in such a
CC manner that at least one circular surface region with a area of 800
CC Angstrom ^2 comprises no mutation. Also included are a composition
CC comprising two or more of the recombinant allergens, where the variant
CC allergen is defined by having at least one primary mutation, which is
CC absent in at least one of the other variants, and for each variant no
CC secondary mutation is present within a radius of 15 Angstrom from each
CC absent primary mutation; a DNA sequence encoding the recombinant allergen
CC or its derivative, partial sequence or degenerated sequence, or a
CC sequence which hybridises to it under stringent conditions, where the
CC derivative, partial sequence, degenerated sequence or hybridising
CC sequence encodes a peptide having at least one B cell epitope; an
CC expression vector comprising the DNA and a host cell comprising the
CC vector. The recombinant allergen is useful as a pharmaceutical, for
CC preparing a pharmaceutical for preventing and/or treating allergy, or in
CC a diagnostic assay for assessing relevance, safety or outcome of therapy
CC of a subject, where an IgE containing sample of the subject is mixed with
CC the recombinant allergen and assessed for the level of reactivity between
CC the IgE in the sample and the recombinant allergen. The recombinant
CC allergen or compositions are useful for generating an immune response in
CC a subject, for vaccination or treatment of a subject or for the
CC treatment, prevention or alleviation of allergic reactions in a subject
CC e.g. hay fever, rhinoconductivitis, rhinitis, asthma or systemic
CC anaphylaxis. The present sequence represents an isoform of the house dust
CC mite allergen Der p 2
XX
SQ Sequence 129 AA;

Query Match 93.4%; Score 646; DB 5; Length 129;
Best Local Similarity 93.0%; Pred. No. 3.9e-68;
Matches 120; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              |||||||||||||:||||||||:||||| |||||||||||||||| ||||||||||||
Db          1 DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEALFEANQNSKTAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | |||||||||||||| |||| |||||||||||||||| ||||||||||:|||||||||
Db         61 LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVMGDNGVLACA 120

Qy        121 IATHAKIRD 129
              |||||||||
Db        121 IATHAKIRD 129
```

RESULT 15
ABG66994
ID ABG66994 standard; protein; 129 AA.
XX
AC ABG66994;
XX
DT 24-SEP-2002 (first entry)
XX
DE House dust mite allergen Der p 2 isoform ALK-104.
XX
KW Immunoglobulin E; IgE; allergen; allergy; hay fever; house dust mite;

KW rhinoconductivitis; rhinitis; asthma; systemic anaphylaxis; isoform;
KW vaccine; antiallergic; B cell epitope; Der p 2.
XX
OS Dermatophagoides pteronyssinus.
XX
PN WO200240676-A2.
XX
PD 23-MAY-2002.
XX
PF 16-NOV-2001; 2001WO-DK000764.
XX
PR 16-NOV-2000; 2000DK-00001718.
PR 16-NOV-2000; 2000US-0249361P.
PR 14-JUN-2001; 2001US-0298170P.
XX
PA (ALKA-) ALK-ABELLO AS.
XX
PI Holm J, Ipsen H, Nedergaard Larsen J, Spangfort MD;
XX
DR WPI; 2002-508328/54.
XX
PT New recombinant mutant allergen, useful for preventing and/or treating
PT allergy, comprises multiple mutations and reduced immunoglobulin E
PT binding affinity.
XX
PS Example 5; Page; 210pp; English.
XX
CC The invention relates to a recombinant allergen (I) which is a mutant of
CC a naturally occurring allergen, where the mutant allergen has at least
CC four primary mutations, which each reduce the specific immunoglobulin E
CC (IgE) binding capability of the mutated allergen as compared to the IgE
CC binding capability of the naturally occurring allergen, where each
CC primary mutation is a substitution of one surface-exposed amino acid
CC residue with another residue, which does not occur in the same position
CC in the amino acid sequence of any known homologous protein within the
CC taxonomic species from which the naturally occurring allergen originates,
CC and each primary mutation is spaced from each other primary mutation by
CC at least 15 Angstrom , and the primary mutations are placed in such a
CC manner that at least one circular surface region with a area of 800
CC Angstrom ^2 comprises no mutation. Also included are a composition
CC comprising two or more of the recombinant allergens, where the variant
CC allergen is defined by having at least one primary mutation, which is
CC absent in at least one of the other variants, and for each variant no
CC secondary mutation is present within a radius of 15 Angstrom from each
CC absent primary mutation; a DNA sequence encoding the recombinant allergen
CC or its derivative, partial sequence or degenerated sequence, or a
CC sequence which hybridises to it under stringent conditions, where the
CC derivative, partial sequence, degenerated sequence or hybridising
CC sequence encodes a peptide having at least one B cell epitope; an
CC expression vector comprising the DNA and a host cell comprising the
CC vector. The recombinant allergen is useful as a pharmaceutical, for
CC preparing a pharmaceutical for preventing and/or treating allergy, or in
CC a diagnostic assay for assessing relevance, safety or outcome of therapy
CC of a subject, where an IgE containing sample of the subject is mixed with
CC the recombinant allergen and assessed for the level of reactivity between
CC the IgE in the sample and the recombinant allergen. The recombinant
CC allergen or compositions are useful for generating an immune response in
CC a subject, for vaccination or treatment of a subject or for the
CC treatment, prevention or alleviation of allergic reactions in a subject
CC e.g. hay fever, rhinoconductivitis, rhinitis, asthma or systemic
CC anaphylaxis. The present sequence represents an isoform of the house dust
CC mite allergen Der p 2
XX
SQ Sequence 129 AA;

Query Match 92.9%; Score 643; DB 5; Length 129;
Best Local Similarity 92.2%; Pred. No. 8.8e-68;
Matches 119; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||:||||||||:|||||  ||||||||||:|||||||  ||||||||||||
Db          1 DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNSKTAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | ||||||||||||||| |||| |||||||||||||||||| ||||||||||:|||||||||
Db         61 LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVIGDNGVLACA 120

Qy        121 IATHAKIRD 129
              |||||||||
Db        121 IATHAKIRD 129
```

Search completed: September 9, 2005, 15:21:35
Job time : 80 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 9, 2005, 15:10:19 ; Search time 24 Seconds
(without alignments)
517.165 Million cell updates/sec

Title: US-10-001-245C-36
Perfect score: 692
Sequence: 1 DQVDVKDCANHEIKEVLVPG.....VLGDNGVLACAIATHAKIRD 129

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	635	91.8	146	2	A60381	allergen Der p II
2	592	85.5	129	2	JU0394	allergen Der f II
3	590	85.3	138	2	B61241	allergen Der f II
4	588	85.0	138	2	A61241	allergen Der f II
5	585	84.5	129	2	A61501	allergen Der f II
6	240.5	34.8	141	2	S66500	allergen Lep d 1.0
7	228.5	33.0	141	2	S66499	allergen Lep d 1.0
8	112	16.2	151	2	I53929	epididymal secreto
9	112	16.2	151	2	I38365	epididymal secreto
10	104.5	15.1	149	2	I69229	epididymal secreto
11	95.5	13.8	186	2	T32408	hypothetical prote
12	84.5	12.2	408	2	G83893	hypothetical prote
13	83	12.0	151	2	A64503	conserved hypothet
14	77.5	11.2	621	2	A75101	aldehyde-ferredoxi
15	77.5	11.2	862	2	T07775	lipoxygenase (EC 1
16	76.5	11.1	6805	2	S20901	titin - rabbit (fr
17	76	11.0	983	2	H64587	cag pathogenicity
18	76	11.0	983	2	F71926	cag pathogenicity
19	75.5	10.9	423	1	VHWVSB	structural polypro
20	75.5	10.9	1245	1	VHWVB2	structural polypro
21	75	10.8	249	2	S75749	hypothetical prote
22	74.5	10.8	625	2	G71072	aldehyde-ferredoxi
23	74.5	10.8	1068	2	F84614	probable kinesin h
24	74	10.7	173	2	S67579	probable membrane
25	73.5	10.6	410	2	C96803	hypothetical prote
26	73	10.5	1098	2	JQ2209	helicase homolog g
27	72.5	10.5	1245	1	VHWV82	structural polypro
28	72.5	10.5	1878	2	E86189	hypothetical prote
29	72.5	10.5	26926	1	I38344	titin, cardiac mus
30	72	10.4	862	2	S57964	lipoxygenase (EC 1
31	72	10.4	1026	2	T34506	hypothetical prote
32	71	10.3	1324	2	T00386	hypothetical prote
33	70.5	10.2	147	2	S77485	ribosomal protein
34	70	10.1	238	2	AC2485	hypothetical prote
35	69.5	10.0	558	2	F64402	vanadate-senstive
36	69.5	10.0	585	2	C70341	acetolactate synth
37	69	10.0	343	1	DEBYMP	malate dehydrogena
38	69	10.0	896	2	AB1156	conserved membrane
39	69	10.0	896	2	AE1514	conserved membrane
40	68.5	9.9	289	2	T28311	ORF MSV150 probabl
41	68.5	9.9	357	2	AC3645	flagellar p-ring p
42	68.5	9.9	385	2	T26487	hypothetical prote
43	68.5	9.9	535	2	AF0103	probable sulfatase
44	68.5	9.9	831	2	AB3513	ATPase virB4 homol
45	68.5	9.9	1245	1	VHWVB	structural polypro

ALIGNMENTS

RESULT 1
A60381
allergen Der p II precursor - house-dust mite (Dermatophagoides pteronyssinus)
C;Species: Dermatophagoides pteronyssinus
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C;Accession: A60381
R;Chua, K.Y.; Doyle, C.R.; Simpson, R.J.; Turner, K.J.; Stewart, G.A.; Thomas, W.R.
Int. Arch. Allergy Appl. Immunol. 91, 118-123, 1990
A;Title: Isolation of cDNA coding for the major mite allergen Der p II by IgE plaque im
A;Reference number: A60381; MUID:90256301; PMID:2341191
A;Accession: A60381
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-146 <CHU>
A;Cross-references: UNIPROT:P49278
C;Superfamily: allergen Der p II
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-146/Product: allergen Der p II #status predicted <MAT>

Query Match 91.8%; Score 635; DB 2; Length 146;
Best Local Similarity 90.7%; Pred. No. 5e-57;
Matches 117; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              |||||||||||||:||||||||:||||| |||||||||:||||||: ||||||||||||
Db         18 DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNTKTAKIEIKASIDG 77

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | |||||||||||||| |||| |||||||||||||||| ||||||||||:||:||||||
Db         78 LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVMGDDGVLACA 137

Qy        121 IATHAKIRD 129
              |||||||||
Db        138 IATHAKIRD 146
```

RESULT 2
JU0394
allergen Der f II (pFL2) - house-dust mite (Dermatophagoides farinae)
C;Species: Dermatophagoides farinae
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 17-Mar-1999
C;Accession: JU0394
R;Yuuki, T.; Okumura, Y.; Ando, T.; Yamakawa, H.; Suko, M.; Haida, M.; Okudaira, H.
Agric. Biol. Chem. 55, 1233-1238, 1991
A;Title: Cloning and expression of cDNA coding for the major house dust mite allergen D
A;Reference number: PS0417; MUID:91291341; PMID:1368682
A;Accession: JU0394
A;Molecule type: mRNA
A;Residues: 1-129 <YUU>
C;Superfamily: allergen Der p II

Query Match 85.5%; Score 592; DB 2; Length 129;

```
  Best Local Similarity   82.9%;  Pred. No. 9.8e-53;
  Matches  107;  Conservative   12;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||:|||:|:| ||||::|||| ||||| |||||:|||| |||||||||:||
Db          1 DQVDVKDCANNEIKKVMVDGCHGSDPCIIHRGKPFTLEALFDANQNTKTAKIEIKASLDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | :|||||| ||||:| |||| |||||||||||||||| |||||||||::|||||||||
Db         61 LEIDVPGIDTNACHFMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKLIGDNGVLACA 120

Qy        121 IATHAKIRD 129
              |||| ||||
Db        121 IATHGKIRD 129


RESULT 3
B61241
allergen Der f II precursor - house-dust mite (Dermatophagoides farinae) (fragment)
C;Species: Dermatophagoides farinae
C;Date: 12-May-1994 #sequence_revision 27-Jun-1994 #text_change 13-Sep-1998
C;Accession: B61241; JU0395
R;Yuuki, T.; Okumura, Y.; Ando, T.; Yamakawa, H.; Suko, M.; Haida, M.; Dohi, M.; Okudair
Int. Arch. Allergy Appl. Immunol. 94, 354-356, 1991
A;Title: Synthesis of biologically active recombinant Der f II.
A;Reference number: A61241; MUID:92040281; PMID:1937898
A;Accession: B61241
A;Molecule type: mRNA
A;Residues: 1-138 <YUU>
C;Superfamily: allergen Der p II
F;1-9/Domain: signal sequence (fragment) #status predicted <SIG>
F;10-138/Product: allergen Der f II #status predicted <MAT>

  Query Match             85.3%;  Score 590;  DB 2;  Length 138;
  Best Local Similarity   82.9%;  Pred. No. 1.7e-52;
  Matches  107;  Conservative   12;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||:|||:|:| ||||::|||| ||||| |||||:|||| |||||||||:||
Db         10 DQVDVKDCANNEIKKVMVDGCHGSDPCIIHRGKPFTLEALFDANQNTKTAKIEIKASLDG 69

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | :|||||| ||||:| |||| ||||| |||||||||||| |||||||||::|||||||||
Db         70 LEIDVPGIDTNACHFMKCPLVKGQQYDAKYTWNVPKIAPKSENVVVTVKLVGDNGVLACA 129

Qy        121 IATHAKIRD 129
              |||||||||
Db        130 IATHAKIRD 138


RESULT 4
A61241
allergen Der f II precursor - house-dust mite (Dermatophagoides farinae) (fragment)
C;Species: Dermatophagoides farinae
C;Date: 12-May-1994 #sequence_revision 27-Jun-1994 #text_change 13-Sep-1998
C;Accession: A61241; PS0417
R;Yuuki, T.; Okumura, Y.; Ando, T.; Yamakawa, H.; Suko, M.; Haida, M.; Dohi, M.; Okudair
Int. Arch. Allergy Appl. Immunol. 94, 354-356, 1991
A;Title: Synthesis of biologically active recombinant Der f II.
A;Reference number: A61241; MUID:92040281; PMID:1937898
A;Accession: A61241
A;Molecule type: mRNA
A;Residues: 1-138 <YUU>
A;Note: part of this seqeunce, including the amino end of the mature protein, was confir
C;Superfamily: allergen Der p II
F;1-9/Domain: signal sequence (fragment) #status predicted <SIG>
F;10-138/Product: allergen Der f II #status experimental <MAT>

  Query Match             85.0%;  Score 588;  DB 2;  Length 138;
  Best Local Similarity   82.2%;  Pred. No. 2.7e-52;
  Matches  106;  Conservative   13;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||:|||:|:| ||||::|||| ||||| |||||:|||| |||||||||:||
Db         10 DQVDVKDCANNEIKKVMVDGCHGSDPCIIHRGKPFTLEALFDANQNTKTAKIEIKASLDG 69

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | :|||||| ||||:| |||| ||||| |||||||||||| |||||||||::|||||||||
Db         70 LEIDVPGIDTNACHFVKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKLIGDNGVLACA 129

Qy        121 IATHAKIRD 129
              |||| ||||
Db        130 IATHGKIRD 138


RESULT 5
A61501
allergen Der f II - house-dust mite (Dermatophagoides farinae) (fragment)
C;Species: Dermatophagoides farinae
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: A61501
R;Trudinger, M.; Chua, K.Y.; Thomas, W.R.
Clin. Exp. Allergy 21, 33-37, 1991
A;Title: cDNA encoding the major mite allergen Der f II.
A;Reference number: A61501; MUID:91215495; PMID:2021876
A;Accession: A61501
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-129 <TRU>
A;Cross-references: UNIPROT:Q8WQK5
C;Superfamily: allergen Der p II

  Query Match             84.5%;  Score 585;  DB 2;  Length 129;
  Best Local Similarity   82.2%;  Pred. No. 5e-52;
  Matches  106;  Conservative   12;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||:|||:|:| ||||::|||| ||||| |||||:|||| ||| |||||:||
Db          1 DQVDVKDCANNEIKKVMVDGCHGSDPCIIHRGKPFTLEALFDANQNTKTAKTEIKASLDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | :|||||| ||||:| |||| ||||| |||||||||||| |||||||||::|||||||||
Db         61 LEIDVPGIDTNACHFMKCPLVKGQQYDAKYTWNVPKIAPKSENVVVTVKLVGDNGVLACA 120

Qy        121 IATHAKIRD 129
              |||||||||
Db        121 IATHAKIRD 129


RESULT 6
S66500
allergen Lep d 1.01 precursor (clone d 1.0102) - Lepidoglyphus destructor
C;Species: Lepidoglyphus destructor
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S66500; S48727; S56034
R;Schmidt, M.; Olsson, S.; van der Ploeg, I.; van Hage-Hamsten, M.
FEBS Lett. 370, 11-14, 1995
A;Title: cDNA analysis of the mite allergen Lep d 1 identifies two different isoallergen
A;Reference number: S66499; MUID:95377437; PMID:7649288
A;Accession: S66500
A;Molecule type: mRNA
A;Residues: 1-141 <SCH>
A;Cross-references: UNIPROT:P80384; EMBL:X89014; NID:g999461; PIDN:CAA61419.1; PID:g9994
R;Varela, J.; Ventas, P.; Carreira, J.; Barbas, J.A.; Gimenez-Gallego, G.; Polo, F.
Eur. J. Biochem. 225, 93-98, 1994
A;Title: Primary structure of Lep d I, the main Lepidoglyphus destructor allergen.
A;Reference number: S48727; MUID:95010146; PMID:7925475
A;Accession: S48727
A;Molecule type: mRNA
A;Residues: 44-141 <VAW>
A;Cross-references: EMBL:X81399; NID:g587449; PIDN:CAA57160.1; PID:g587450
A;Accession: S56034
A;Molecule type: protein
A;Residues: 17-140 <VAR>
A;Note: 53-Asp, 63-Asn, 95-Ile, 104-Asn, 106-Gly and 125-Val were also found
C;Superfamily: allergen Der p II
```

```
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-140/Product: allergen Lep d 1.01 #status experimental <MAT>

  Query Match            34.8%;  Score 240.5;  DB 2;  Length 141;
  Best Local Similarity  36.1%;  Pred. No. 4.3e-17;
  Matches   44;  Conservative   31;  Mismatches   44;  Indels    3;  Gaps    3;

Qy          6 KDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDGLSVDV 65
              ||| : |: |: : || | : |:| ||:   ||| | |||::|   |:: | : | :: |
Db         22 KDCGHGEVTELDITGCSG-DTCVIHRGEKMTLEAKFAANQDTAKVTIKVLAKVAGTTIQV 80

Qy         66 PGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACAIATHA 125
              ||:: : | :: ||:  |:  | |:  :| | |  :   || :::||:||:||    |
Db         81 PGLETDGCKFIKCPVKKGEALDFIYSGTIPAITPKVK-ADVTAELIGDHGVMACG-TVHG 138

Qy        126 KI 127
              ::
Db        139 QV 140


RESULT 7
S66499
allergen Lep d 1.02 precursor - Lepidoglyphus destructor
C;Species: Lepidoglyphus destructor
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 29-Sep-1999
C;Accession: S66499
R;Schmidt, M.; Olsson, S.; van der Ploeg, I.; van Hage-Hamsten, M.
FEBS Lett. 370, 11-14, 1995
A;Title: cDNA analysis of the mite allergen Lep d 1 identifies two different isoallergen
A;Reference number: S66499; MUID:95377437; PMID:7649288
A;Accession: S66499
A;Molecule type: mRNA
A;Residues: 1-141 <SCH>
A;Cross-references: EMBL:X83875; NID:g999457; PIDN:CAA58755.1; PID:g999458
C;Superfamily: allergen Der p II
F;1-16/Domain: signal sequence #status predicted <SIG>
F;17-141/Product: allergen Lep d 1.02 #status predicted <MAT>

  Query Match            33.0%;  Score 228.5;  DB 2;  Length 141;
  Best Local Similarity  34.4%;  Pred. No. 7e-16;
  Matches   42;  Conservative   30;  Mismatches   47;  Indels    3;  Gaps    3;

Qy          6 KDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDGLSVDV 65
              ||| : |: |: : || | : |:| ||:   |:| | |||::   |:: | : | :: |
Db         22 KDCGHGEVTELDISGCSG-DTCVIHRGQKMTLDAKFAANQDTNKVTIKVLAKVAGTTIQV 80

Qy         66 PGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACAIATHA 125
              ||:: : |  : ||:  |:  | |  :| | |  :   || :::||:||:||    |
Db         81 PGLETDGCKVLKCPIKKGEALDFNYGMTIPAITPKIK-ADVTAELVGDHGVMACG-TIHG 138

Qy        126 KI 127
              ::
Db        139 QV 140


RESULT 8
I53929
epididymal secretory protein 14.6 - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I53929
R;Perry, A.C.; Jones, R.; Hall, L.
Gene 153, 291-292, 1995
A;Title: The monkey ESP14.6 mRNA, a novel transcript expressed at high levels in the epi
A;Reference number: I53929; MUID:95180740; PMID:7875608
A;Accession: I53929
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-151 <RES>
A;Cross-references: UNIPROT:P61918; EMBL:X78134; NID:g794070; PIDN:CAA55013.1; PID:g7940
C;Superfamily: allergen Der p II

  Query Match            16.2%;  Score 112;  DB 2;  Length 151;
  Best Local Similarity  29.1%;  Pred. No. 0.00048;
  Matches   37;  Conservative   26;  Mismatches   50;  Indels   14;  Gaps    7;

Qy          1 DQVDVKDCANHE--IKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASI 58
              : |  ||| : :  |||| |  |   :|| : :|: : :   | :|  | ::|  :   :
Db         20 EPVQFKDCGSVDGVIKEVNVSPC-PTQPCQLSKGQSYSVNVTFTSNIQSKSSKAVVHGIL 78

Qy         59 DGLSVDVPGIDPNACHY-MNCPLVNGQQYDIKYTWNVPKIAPNSE----NVVVTVKVLGD 113
              |: |  |  :|: |   :|||:    | |  |:: : |:   ||     :||  ::  |
Db         79 MGVPVPFPIPEPDGCKSGINCPI----QKDKTYSY-LNKLPVKSEYPSIKLVVEWQLQDD 133

Qy        114 -NGVLAC 119
               | | |
Db        134 KNQSLFC 140


RESULT 9
I38365
epididymal secretory protein - human
C;Species: Homo sapiens (man)
C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: I38365; S25641
R;Krull, N.; Ivell, R.; Osterhoff, C.; Kirchhoff, C.
Mol. Reprod. Dev. 34, 16-24, 1993
A;Title: Region-specific variation of gene expression in the human epididymis as reveal
A;Reference number: I38365; MUID:93119659; PMID:8418812
A;Accession: I38365
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-151 <RES>
A;Cross-references: UNIPROT:P61916; EMBL:X67698; NID:g37476; PIDN:CAA47928.1; PID:g3747
A;Note: submitted to the EMBL Data Library, August 1992
C;Superfamily: allergen Der p II

  Query Match            16.2%;  Score 112;  DB 2;  Length 151;
  Best Local Similarity  29.1%;  Pred. No. 0.00048;
  Matches   37;  Conservative   26;  Mismatches   50;  Indels   14;  Gaps    7;

Qy          1 DQVDVKDCANHE--IKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASI 58
              : |  ||| : :  |||| |  |   :|| : :|: : :   | :|  | ::|  :   :
Db         20 EPVQFKDCGSVDGVIKEVNVSPC-PTQPCQLSKGQSYSVNVTFTSNIQSKSSKAVVHGIL 78

Qy         59 DGLSVDVPGIDPNACHY-MNCPLVNGQQYDIKYTWNVPKIAPNSE----NVVVTVKVLGD 113
              |: |  |  :|: |   :|||:    | |  |:: : |:   ||     :||  ::  |
Db         79 MGVPVPFPIPEPDGCKSGINCPI----QKDKTYSY-LNKLPVKSEYPSIKLVVEWQLQDD 133

Qy        114 -NGVLAC 119
               | | |
Db        134 KNQSLFC 140


RESULT 10
I69229
epididymal secretory protein CE1 - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C;Accession: I69229
R;Ellerbrock, K.; Pera, I.; Hartung, S.; Ivell, R.
Int. J. Androl. 17, 314-323, 1994
A;Title: Gene expression in the dog epididymis: a model for human epididymal function.
A;Reference number: I54768; MUID:95263175; PMID:7744511
A;Accession: I69229
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-149 <ELL>
A;Cross-references: UNIPROT:Q28895; GB:S77411; NID:g945178; PIDN:AAB34263.1; PID:g94517
C;Genetics:
A;Gene: GDB:HE1
A;Cross-references: GDB:9957680
C;Superfamily: allergen Der p II

  Query Match            15.1%;  Score 104.5;  DB 2;  Length 149;
  Best Local Similarity  30.2%;  Pred. No. 0.0027;
```

```
  Matches   35;  Conservative   22;  Mismatches   52;  Indels    7;  Gaps    5;

Qy          3 VDVKDC--ANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              |  |||  |   |||: |  |   :|| : :|: : :   | :|  | ::|  :   : |
Db         22 VHFKDCGSAVGVIKELNVNPCPA-QPCKLHKGQSYSVNVTFTSNIPSQSSKAVVHGIVLG 80

Qy         61 LSVDVPGIDPNACHY-MNCPLVNGQQYDIKYTWNVP-KIAPNSENVVVTVKVLGDN 114
              ::|  |  : : |   :|||:   : |   |  :| |    |  :||   :||||
Db         81 VAVPFPIPEADGCKSGINCPIQKDKTY--SYLNKLPVKNEYPSIKLVVQWMLLGDN 134


RESULT 11
T32408
hypothetical protein R148.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32408
R;Le, T.T.; Kemp, K.; Scheet, P.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid R148.
A;Reference number: Z21161
A;Accession: T32408
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-186 <LET>
A;Cross-references: UNIPROT:O17271; EMBL:AF025467; PIDN:AAB71040.1; GSPDB:GN00021; CESP:
A;Experimental source: strain Bristol N2; clone R148
C;Genetics:
A;Gene: CESP:R148.6
A;Map position: 3
A;Introns: 32/2; 132/1

  Query Match             13.8%;  Score 95.5;  DB 2;  Length 186;
  Best Local Similarity   21.7%;  Pred. No. 0.029;
  Matches   28;  Conservative   34;  Mismatches   58;  Indels    9;  Gaps    5;

Qy          2 QVDVKDC-ANHEIKEVLVPGCH-----GNEPCIIGRGKPFQLEALFEANQNSATAKIEIK 55
              ::  | | ::  : :|   ||       | : |:  :|    ::   |: ::::   |  ::
Db         51 EIGYKVCKSDGTVSQVKADGCELTVKDGKKVCLFKKGSRPIIQIAFKPSKDTDKLKTSVR 110

Qy         56 ASIDGLS-VDVPGIDPNACHY-MNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVL-G 112
              | : | : || |  : :|| | : ||:  |:    : : :: :  |  | : |  ::
Db        111 AKVGGSAMVDFPQTNSDACTYGVKCPVSAGENQIFEQSISITENHPAGEVIQVNWQLTRP 170

Qy        113 DNGVLACAI 121
              |:|   | |
Db        171 DSGKEVCII 179


RESULT 12
G83893
hypothetical protein BH1951 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: G83893
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83893
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-408 <STO>
A;Cross-references: UNIPROT:Q9KBH6; GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BAB056
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH1951

  Query Match             12.2%;  Score 84.5;  DB 2;  Length 408;
  Best Local Similarity   28.9%;  Pred. No. 0.93;
  Matches   35;  Conservative   19;  Mismatches   40;  Indels   27;  Gaps    7;

Qy         34 PFQL-----EALFEANQNSATAKIEIKASIDG-LSVDVPGIDP----------NACHYMN 77
              || |       : :| ::    ::  :  ||  || :| || |          | ||:||
Db         83 PFTLGHEMVGTISKARKSVTNLQVGQRVVIDPLLSCEVRGITPVCSECANGNYNLCHHMN 142

Qy         78 ----CP-LVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVL----ACAIATHAKIR 128
                  | |: |   |   :|    :|  |: : :   |  |||||    |||:  || ::
Db        143 DGDIAPGLLTGTCKDTGGSWGRYLVAHQSQVISLPSSVDDDNGVLVEPFACAL--HAVLQ 200

Qy        129 D 129
              :
Db        201 N 201


RESULT 13
A64503
conserved hypothetical protein MJ1627 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: A64503
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese,
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschi
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: A64503
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-151 <BUL>
A;Cross-references: UNIPROT:Q59021; GB:U67602; GB:L77117; NID:g1592214; PIDN:AAB99644.1,
C;Genetics:
A;Map position: REV1604684-1604229
C;Superfamily: uncharacterized conserved protein

  Query Match             12.0%;  Score 83;  DB 2;  Length 151;
  Best Local Similarity   21.3%;  Pred. No. 0.41;
  Matches   29;  Conservative   22;  Mismatches   49;  Indels   36;  Gaps    5;

Qy          4 DVKDCANHEIKEVLVPGCHG----------------NEPCIIGRGKPFQLEALFEANQNS 47
              ::::| | : | :    |||                 | |||:  |    :| :
Db         26 EIEECKNCKFKRL----CHGNLEVGRKYKIVSVRSANHPCIVHEGGVKVVEVVLA----D 77

Qy         48 ATAKIEIKASIDGLSVDVPGIDPNACHYMNCP---------LVNGQQYDIKYTWNVPKIA 98
                |  || | :::|:   |   :|  |   :|          :  |::| ||   |
Db         78 LTIMIESKKALEGV---VLNHEPITCDNFDCEYYSFCNSEGIKEGEKYKIKQVLNEKINC 134

Qy         99 PNSENVVVTVKVLGDN 114
              |   ::   :  | :|
Db        135 PFGNSLKKVIVELVEN 150


RESULT 14
A75101
aldehyde-ferredoxin oxidoreductase (EC 1.-.-.-) PAB0798 [imported] - Pyrococcus abyssi (
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: A75101
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: A75101
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-621 <KAW>
A;Cross-references: UNIPROT:Q9UZE9; GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB5011
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: for; PAB0798
C;Superfamily: probable aldehyde ferredoxin oxidoreductase aor-4
C;Keywords: oxidoreductase

  Query Match             11.2%;  Score 77.5;  DB 2;  Length 621;
```

```
  Best Local Similarity   23.7%;  Pred. No. 7.8;
  Matches   33;  Conservative   20;  Mismatches   51;  Indels   35;  Gaps    7;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPF-----QLEALFEANQNSA------- 48
              |: ::|  :     ::|      | |     | ||      : |:   |:|||
Db        211 DKEELKKLSGEAYNDIL------NAP-----GYPFWKRQGTMAAVEWTNENSALPTRNFS 259

Qy         49 TAKIEIKASIDGLSVDVPGIDPNACHYMNCPLVN------GQQYDIKYTWNVPKIAPN-- 100
                |   |||| :::   :    | | | |  |       ||: :: |  ||  :  |
Db        260 DGSFEFARSIDGYTMEGMKVKQRGCPYCNMPCGNVVLDAEGQESELDYE-NVALLGANLG 318

Qy        101 ---SENVVVTVKVLGDNGV 116
                  | |  ::  | |:
Db        319 IGKLNEVAVLNRIADDMGM 337


RESULT 15
T07775
lipoxygenase (EC 1.13.11.12) LX-3 - potato
C;Species: Solanum tuberosum (potato)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
C;Accession: T07775
R;Kolomiets, M.V.; Hannapel, D.J.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z16124
A;Accession: T07775
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-862 <KOL>
A;Cross-references: UNIPROT:Q43191; EMBL:U60202; NID:g1407704; PIDN:AAB67865.1; PID:g140
A;Experimental source: cv. Berolina
C;Genetics:
A;Gene: LX-3
C;Function:
A;Description: catalyzes the oxidation of unsaturated fatty acids with a 1,4-cis,cis pen
C;Superfamily: lipoxygenase
C;Keywords: fatty acid oxidation; oxidoreductase

  Query Match             11.2%;  Score 77.5;  DB 2;  Length 862;
  Best Local Similarity   30.1%;  Pred. No. 11;
  Matches   31;  Conservative   18;  Mismatches   35;  Indels   19;  Gaps    6;

Qy         23 GNEPCIIGRGKPF----QLEALFEANQNSATAKIEIKASIDGLSVDVPGIDPNACHYMNC 78
              |  | || | : |    ||::    ||||   |  |: ::|||::|   |  |  : :|
Db        376 GVNPVIISRLQEFPPKSQLDSEVYGNQNSTITKEHIENTLDGLTID-DAIKTNRLYILN- 433

Qy         79 PLVNGQQYDIKYTWNVPKIAPNSENVVV----TVKVLGDNGVL 117
                    :||   : | :|  |: |  :    |:  | |:| :
Db        434 ------HHDILMPY-VRRI--NTTNTKLYASRTLLFLQDDGTM 467


Search completed: September  9, 2005, 15:23:32
Job time : 26 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 9, 2005, 15:09:49 ; Search time 80 Seconds
(without alignments)
825.728 Million cell updates/sec

Title: US-10-001-245C-36
Perfect score: 692
Sequence: 1 DQVDVKDCANHEIKEVLVPG.....VLGDNGVLACAIATHAKIRD 129

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	635	91.8	146	1	ALL2_DERPT	P49278 dermatophag
2	592	85.5	146	1	ALL2_DERFA	Q00855 dermatophag
3	590	85.3	129	2	Q8WQK5	Q8wqk5 dermatophag
4	575	83.1	145	1	ALL2_EURMA	Q9tzz2 euroglyphus
5	567.5	82.0	170	2	Q9BIX2	Q9bix2 dermatophag
6	272.5	39.4	143	1	ALL2_PSOOV	Q965e2 psoroptes o
7	251	36.3	125	1	AL22_GLYDO	Q9nfq4 glycyphagus
8	246.5	35.6	141	1	ALL2_TYRPU	O02380 tyrophagus
9	243	35.1	128	1	AL21_GLYDO	Q9u5p7 glycyphagus
10	240.5	34.8	141	1	ALL2_LEPDS	P80384 lepidoglyph
11	122.5	17.7	163	2	Q7QCX5	Q7qcx5 anopheles g
12	117	16.9	151	2	Q66K95	Q66k95 xenopus tro
13	115.5	16.7	149	1	NPC2_PIG	O97763 sus scrofa
14	112	16.2	151	1	NPC2_HUMAN	P61916 homo sapien
15	112	16.2	151	1	NPC2_MACFA	P61918 macaca fasc
16	112	16.2	151	1	NPC2_PANTR	P61917 pan troglod
17	106	15.3	150	2	Q6PAA7	Q6paa7 xenopus lae
18	106	15.3	151	2	Q6NTT7	Q6ntt7 xenopus lae
19	104.5	15.1	149	1	NPC2_CANFA	Q28895 canis famil
20	104	15.0	148	2	Q64FT1	Q64ft1 gekko japon
21	100.5	14.5	149	1	NPC2_BOVIN	P79345 bos taurus
22	96	13.9	158	2	Q7QCX4	Q7qcx4 anopheles g
23	95.5	13.8	154	1	Y146_CAEEL	O17271 caenorhabdi
24	95	13.7	149	1	NPC2_MOUSE	Q9z0j0 mus musculu
25	92.5	13.4	116	2	Q86GB5	Q86gb5 ixodes rici
26	92.5	13.4	155	2	Q7YZR7	Q7yzr7 ixodes rici
27	91.5	13.2	149	2	Q8CHN5	Q8chn5 rattus norv
28	90.5	13.1	165	2	Q9VH31	Q9vh31 drosophila
29	89.5	12.9	149	1	NPC2_BRARE	Q9dgj3 brachydanio
30	87	12.6	148	1	NPC2_DROME	Q9vq62 drosophila
31	84.5	12.2	153	2	Q7QCX6	Q7qcx6 anopheles g
32	84.5	12.2	408	2	Q9KBH6	Q9kbh6 bacillus ha
33	83	12.0	151	1	YG27_METJA	Q59021 methanococc
34	82	11.8	159	2	Q9VFN7	Q9vfn7 drosophila
35	81	11.7	153	2	Q7QCX8	Q7qcx8 anopheles g
36	79.5	11.5	137	2	Q7Q0A4	Q7q0a4 anopheles g
37	79.5	11.5	414	2	Q9JHX6	Q9jhx6 mus musculu
38	79	11.4	164	2	Q7PZQ2	Q7pzq2 anopheles g
39	79	11.4	188	2	Q7PZQ3	Q7pzq3 anopheles g
40	79	11.4	422	2	Q8K053	Q8k053 mus musculu
41	79	11.4	711	2	Q8CBC4	Q8cbc4 mus musculu
42	77.5	11.2	214	2	Q6TR70	Q6tr70 pythium aff
43	77.5	11.2	214	2	Q6TR71	Q6tr71 pythium mid
44	77.5	11.2	214	2	Q6TR72	Q6tr72 pythium mon
45	77.5	11.2	273	2	Q72ER8	Q72er8 desulfovibr

ALIGNMENTS

RESULT 1
ALL2_DERPT
ID ALL2_DERPT STANDARD; PRT; 146 AA.
AC P49278;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Mite group 2 allergen Der p 2 precursor (Der p II) (DPX).
GN Name=DERP2;
OS Dermatophagoides pteronyssinus (House-dust mite).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;
OC Pyroglyphidae; Dermatophagoides.
OX NCBI_TaxID=6956;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90256301; PubMed=2341191;
RA Chua K.Y., Doyle C.R., Simpson R.J., Turner K.J., Stewart G.A.,
RA Thomas W.R.;
RT "Isolation of cDNA coding for the major mite allergen Der p II by IgE
RT plaque immunoassay.";
RL Int. Arch. Allergy Appl. Immunol. 91:118-123(1990).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANTS.
RX MEDLINE=21290932; PubMed=11398075; DOI=10.1067/mai.2001.114652;
RA Smith W.-A., Hales B.J., Jarnicki A.G., Thomas W.R.;
RT "Allergens of wild house dust mites: environmental Der p 1 and Der p 2
RT sequence polymorphisms.";
RL J. Allergy Clin. Immunol. 107:985-992(2001).
RN [3]
RP PARTIAL SEQUENCE OF 18-57.
RX MEDLINE=89278484; PubMed=2732406;
RA Heymann P.W., Chapman M.D., Aalberse R.C., Fox J.W.,
RA Platts-Mills T.A.;
RT "Antigenic and structural analysis of group II allergens (Der f II and
RT Der p II) from house dust mites (Dermatophagoides spp).";
RL J. Allergy Clin. Immunol. 83:1055-1067(1989).
RN [4]
RP STRUCTURE BY NMR.
RX MEDLINE=98409423; PubMed=9737847; DOI=10.1021/bi980578+;
RA Mueller G.A., Benjamin D.C., Rule G.S.;
RT "Tertiary structure of the major house dust mite allergen Der p 2:
RT sequential and structural homologies.";
RL Biochemistry 37:12707-12714(1998).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALLERGEN: Causes an allergic reaction in human. Common symptoms of
CC mite allergy are bronchial asthma, allergic rhinitis and
CC conjunctivitis.
CC -!- SIMILARITY: Belongs to the NPC2 family.
CC ---

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CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF276239; AAF86462.1; -.
DR   PIR; A60381; A60381.
DR   PDB; 1A9V; NMR; @=18-146.
DR   PDB; 1KTJ; X-ray; A/B=18-146.
DR   InterPro; IPR003172; E1_DerP2_DerF2.
DR   Pfam; PF02221; E1_DerP2_DerF2; 1.
DR   SMART; SM00737; ML; 1.
KW   3D-structure; Allergen; Direct protein sequencing; Polymorphism;
KW   Signal.
FT   SIGNAL        1     17
FT   CHAIN        18    146       Mite group 2 allergen Der p 2.
FT   DISULFID     25    136
FT   DISULFID     38     44
FT   DISULFID     90     95
FT   VARIANT      39     39       H -> A.
FT   VARIANT      40     40       G -> L.
FT   VARIANT      44     44       C -> N.
FT   VARIANT      47     47       H -> S.
FT   VARIANT      49     49       G -> T.
FT   VARIANT      56     56       A -> Y.
FT   VARIANT      57     57       V -> L.
FT   VARIANT      61     61       N -> L.
FT   VARIANT      64     64       T -> S.
FT   VARIANT      75     75       I -> Y.
FT   VARIANT      78     78       L -> C.
FT   VARIANT      81     81       D -> V.
FT   VARIANT      95     95       C -> P.
FT   VARIANT      98     98       V -> T.
FT   VARIANT     108    108       T -> V.
FT   VARIANT     111    111       V -> L.
FT   VARIANT     114    114       I -> N.
FT   VARIANT     115    115       A -> T.
FT   VARIANT     116    116       P -> A.
FT   VARIANT     118    118       S -> A.
FT   VARIANT     127    127       V -> L.
FT   VARIANT     128    128       M -> L.
FT   VARIANT     131    131       D -> N.
FT   VARIANT     133    133       V -> A.
FT   VARIANT     144    144       I -> L.
FT   STRAND       19     20
FT   STRAND       23     24
FT   STRAND       30     34
FT   TURN         36     37
FT   STRAND       40     40
FT   TURN         41     41
FT   STRAND       44     47
FT   TURN         48     49
FT   STRAND       51     59
FT   STRAND       64     64
FT   STRAND       68     75
FT   TURN         76     77
FT   STRAND       78     80
FT   STRAND       88     88
FT   HELIX        89     91
FT   STRAND       97     97
FT   TURN         99    100
FT   STRAND      102    110
FT   TURN        113    114
FT   STRAND      118    118
FT   STRAND      121    129
FT   TURN        130    131
FT   STRAND      132    139
FT   STRAND      142    146
SQ   SEQUENCE   146 AA;  15999 MW;  591B2FA7FD26D3AF CRC64;

  Query Match             91.8%;  Score 635;  DB 1;  Length 146;
  Best Local Similarity   90.7%;  Pred. No. 9.5e-55;
  Matches  117;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||:||||||||:||||| |||||||||:||||||: ||||||||||||
Db         18 DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNTKTAKIEIKASIDG 77

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | ||||||||||||||| |||| |||||||||||||||||| ||||||||||:||:||||||
Db         78 LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVMGDDGVLACA 137

Qy        121 IATHAKIRD 129
              |||||||||
Db        138 IATHAKIRD 146


RESULT 2
ALL2_DERFA
ID   ALL2_DERFA     STANDARD;      PRT;   146 AA.
AC   Q00855; P39672; Q26359;
DT   01-OCT-1993 (Rel. 27, Created)
DT   01-OCT-1993 (Rel. 27, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Mite group 2 allergen Der f 2 precursor (Der f II).
GN   Name=DERF2;
OS   Dermatophagoides farinae (House-dust mite).
OC   Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC   Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;
OC   Pyroglyphidae; Dermatophagoides.
OX   NCBI_TaxID=6954;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX   MEDLINE=91291341; PubMed=1368682;
RA   Yuuki T., Okumura Y., Ando T., Yamakawa H., Suko M., Haida M.,
RA   Okudaira H.;
RT   "Cloning and expression of cDNA coding for the major house dust mite
RT   allergen Der f II in Escherichia coli.";
RL   Agric. Biol. Chem. 55:1233-1238(1991).
RN   [2]
RP   SEQUENCE OF 4-146 FROM N.A.
RX   MEDLINE=94256850; PubMed=8198452;
RA   Okuhira H.;
RT   "Molecular biology of mite antigens.";
RL   Arerugi 43:435-440(1994).
RN   [3]
RP   DISULFIDE BONDS, AND PARTIAL SEQUENCE.
RX   MEDLINE=93283958; PubMed=8508052;
RA   Nishiyama C., Yuuki T., Takai T., Okumura Y., Okudaira H.;
RT   "Determination of three disulfide bonds in a major house dust mite
RT   allergen, Der f II.";
RL   Int. Arch. Allergy Immunol. 101:159-166(1993).
RN   [4]
RP   PARTIAL SEQUENCE OF 18-52.
RX   MEDLINE=89278484; PubMed=2732406;
RA   Heymann P.W., Chapman M.D., Aalberse R.C., Fox J.W.,
RA   Platts-Mills T.A.;
RT   "Antigenic and structural analysis of group II allergens (Der f II and
RT   Der p II) from house dust mites (Dermatophagoides spp).";
RL   J. Allergy Clin. Immunol. 83:1055-1067(1989).
RN   [5]
RP   STRUCTURE BY NMR.
RX   MEDLINE=98079068; PubMed=9417088; DOI=10.1074/jbc.273.1.356;
RA   Ichikawa S., Hatanaka H., Yuuki T., Iwamoto N., Kojima S.,
RA   Nishiyama C., Ogura K., Okumura Y., Inagaki F.;
RT   "Solution structure of Der f 2, the major mite allergen for atopic
RT   diseases.";
RL   J. Biol. Chem. 273:356-360(1998).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- ALLERGEN: Causes an allergic reaction in human. Common symptoms of
CC       mite allergy are bronchial asthma, allergic rhinitis and
CC       conjunctivitis.
CC   -!- MISCELLANEOUS: The sequence shown here is from clone 2. The N-
CC       terminal sequence (AA 1-8) from clone 1 and 11 are not yet known.
CC   -!- SIMILARITY: Belongs to the NPC2 family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   ----------------------------------------------------------------------
DR   EMBL; D10447; BAA01239.1; -.
DR   EMBL; D10448; BAA01240.1; -.
DR   EMBL; D10449; BAA01241.1; -.
DR   EMBL; S70378; AAB30829.1; -.
DR   PDB; 1AHK; NMR; @=18-146.
DR   PDB; 1AHM; NMR; @=18-146.
DR   InterPro; IPR003172; E1_DerP2_DerF2.
DR   Pfam; PF02221; E1_DerP2_DerF2; 1.
DR   SMART; SM00737; ML; 1.
KW   3D-structure; Allergen; Direct protein sequencing; Polymorphism;
KW   Signal.
FT   SIGNAL        1     17
FT   CHAIN        18    146       Mite group 2 allergen Der f 2.
FT   DISULFID     25    136
FT   DISULFID     38     44
FT   DISULFID     90     95
FT   VARIANT      93     93       M -> V (in clone 1).
FT   VARIANT     105    105       I -> A (in clone 11).
FT   VARIANT     128    128       I -> V (in clone 11).
FT   VARIANT     142    142       G -> A (in clone 11).
FT   CONFLICT      5      8       ILCL -> GTMV (in Ref. 2).
FT   STRAND       44     46
FT   STRAND       54     54
FT   STRAND       58     60
FT   STRAND       74     75
FT   TURN         76     77
FT   STRAND       78     78
FT   TURN         98     99
FT   STRAND      101    103
FT   STRAND      107    107
FT   STRAND      122    128
FT   STRAND      133    139
FT   STRAND      142    144
SQ   SEQUENCE   146 AA;  15802 MW;  FA118206CD88534A CRC64;

  Query Match             85.5%;  Score 592;  DB 1;  Length 146;
  Best Local Similarity   82.9%;  Pred. No. 1.7e-50;
  Matches  107;  Conservative   12;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||:|||:|:| ||||::|||| ||||| ||||||:||||: ||||||||||:||
Db         18 DQVDVKDCANNEIKKVMVDGCHGSDPCIIHRGKPFTLEALFDANQNTKTAKIEIKASLDG 77

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | :|||||| ||||:| |||| |||||||||||||||| |||||||||::|||||||||
Db         78 LEIDVPGIDTNACHFMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKLIGDNGVLACA 137

Qy        121 IATHAKIRD 129
               |||| ||||
Db        138 IATHGKIRD 146


RESULT 3
Q8WQK5
ID   Q8WQK5      PRELIMINARY;      PRT;   129 AA.
AC   Q8WQK5;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Major Der f 2 isoform (Fragment).
OS   Dermatophagoides farinae (House-dust mite).
OC   Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC   Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;
OC   Pyroglyphidae; Dermatophagoides.
OX   NCBI_TaxID=6954;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Jin H.S., Oh S.H., Hong C.-S.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY066008; AAL47677.1; -.
DR   PIR; A61501; A61501.
DR   HSSP; Q00855; 1AHK.
DR   Pfam; PF02221; E1_DerP2_DerF2; 1.
DR   SMART; SM00737; ML; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   129 AA;  14035 MW;  832F72E25FE4F43F CRC64;

  Query Match             85.3%;  Score 590;  DB 2;  Length 129;
  Best Local Similarity   82.9%;  Pred. No. 2.3e-50;
  Matches  107;  Conservative   12;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||:|||:|:| ||||::|||| ||||| ||||||:||||: ||||||||||:||
Db          1 DQVDVKDCANNEIKKVMVDGCHGSDPCIIHRGKPFTLEALFDANQNTKTAKIEIKASLDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | :|||||| ||||:| |||| |||||||||||||||| |||||||||::|||||||||
Db         61 LEIDVPGIDTNACHFMKCPLVKGQQYDAKYTWNVPKIAPESENVVVTVKLVGDNGVLACA 120

Qy        121 IATHAKIRD 129
               |||| ||||
Db        121 IATHAKIRD 129


RESULT 4
ALL2_EURMA
ID   ALL2_EURMA     STANDARD;      PRT;   145 AA.
AC   Q9TZZ2; O96430;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Mite group 2 allergen Eur m 2 precursor.
GN   Name=EURM2;
OS   Euroglyphus maynei (Mayne's house dust mite).
OC   Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC   Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;
OC   Pyroglyphidae; Euroglyphus.
OX   NCBI_TaxID=6958;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99126275; PubMed=9925958; DOI=10.1159/000024026;
RA   Smith W., Mills K., Hazell L., Hart B.J., Thomas W.;
RT   "Molecular analysis of the group 1 and 2 allergens from the house dust
RT   mite, Euroglyphus maynei.";
RL   Int. Arch. Allergy Immunol. 118:15-22(1999).
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- POLYMORPHISM: The sequence shown is that of isoform Eur m 2.0101.
CC   -!- ALLERGEN: Causes an allergic reaction in human. Common symptoms of
CC       mite allergy are bronchial asthma, allergic rhinitis and
CC       conjunctivitis.
CC   -!- SIMILARITY: Belongs to the NPC2 family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF047613; AAC82349.1; -.
DR   EMBL; AF047614; AAC82350.1; -.
DR   HSSP; P49278; 1A9V.
DR   InterPro; IPR003172; E1_DerP2_DerF2.
DR   Pfam; PF02221; E1_DerP2_DerF2; 1.
DR   SMART; SM00737; ML; 1.
KW   Allergen; Polymorphism; Signal.
FT   SIGNAL        1     16       Potential.
FT   CHAIN        17    145       Mite group 2 allergen Eur m 2.
```

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FT   DISULFID     24    135       By similarity.
FT   DISULFID     37     43       By similarity.
FT   DISULFID     89     94       By similarity.
FT   VARIANT      21     21       I -> V (in Eur m 2 0102).
SQ   SEQUENCE   145 AA;  15747 MW;  6655B16C8503A565 CRC64;

  Query Match             83.1%;  Score 575;  DB 1;  Length 145;
  Best Local Similarity   79.8%;  Pred. No. 7.9e-49;
  Matches  103;  Conservative   14;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||:|||||||||:|:|||| |:|||:| ||  |||||:|:|||||  |||||||:|||
Db         17 DQVDIKDCANHEIKKVMVPGCKGSEPCVIHRGTAFQLEAVFDANQNSNAAKIEIKATIDG 76

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              : :|||||| | ||:| |||| ||:||||||||||:||| |||||||||:||||||||||
Db         77 VEIDVPGIDNNLCHFMKCPLVKGQEYDIKYTWNVPRIAPKSENVVVTVKLLGDNGVLACA 136

Qy        121 IATHAKIRD 129
              |||||||||
Db        137 IATHAKIRD 145


RESULT 5
Q9BIX2
ID   Q9BIX2      PRELIMINARY;      PRT;   170 AA.
AC   Q9BIX2;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Allergen Def f II (Fragment).
OS   Dermatophagoides farinae (House-dust mite).
OC   Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC   Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;
OC   Pyroglyphidae; Dermatophagoides.
OX   NCBI_TaxID=6954;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hao M., Xu J., Zhong N.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF346905; AAK30133.1; -.
DR   HSSP; Q00855; 1AHK.
DR   InterPro; IPR003172; E1_DerP2_DerF2.
DR   Pfam; PF02221; E1_DerP2_DerF2; 1.
DR   SMART; SM00737; ML; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   170 AA;  18781 MW;  0C2B58734C9D443A CRC64;

  Query Match             82.0%;  Score 567.5;  DB 2;  Length 170;
  Best Local Similarity   67.7%;  Pred. No. 5.2e-48;
  Matches  107;  Conservative   12;  Mismatches   10;  Indels   29;  Gaps    1;

Qy          1 DQVDVKDC----------------------------ANHEIKEVLVPGCHGNEPCIIGR 31
              ||||||||                            ||:|||:|:| ||||::|||| |
Db         13 DQVDVKDCGKFVCVIHFFSFHLFNTKHNFLFLVYIHIANNEIKKVMVDGCHGSDPCIIHR 72

Qy         32 GKPFQLEALFEANQNSATAKIEIKASIDGLSVDVPGIDPNACHYMNCPLVNGQQYDIKYT 91
              |||| |||||:||||: |||||||||:||| :|||||| ||||:| |||| |||||||||
Db         73 GKPFTLEALFDANQNTKTAKIEIKASLDGLEIDVPGIDTNACHFMKCPLVKGQQYDIKYT 132

Qy         92 WNVPKIAPNSENVVVTVKVLGDNGVLACAIATHAKIRD 129
              |||||||| |||||||::|||||||||||||| ||||
Db        133 WNVPKIAPKSENVVVTVKLIGDNGVLACAIATHGKIRD 170


RESULT 6
ALL2_PSOOV
ID   ALL2_PSOOV     STANDARD;      PRT;   143 AA.
AC   Q965E2;
DT   05-JUL-2004 (Rel. 44, Created)
DT   05-JUL-2004 (Rel. 44, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Mite group 2 allergen Pso o 2 precursor (Allergen Pso o A).
GN   Name=ALLA;
OS   Psoroptes ovis (Sheep scab mite).
OC   Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC   Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Sarcoptoidea;
OC   Psoroptidae; Psoroptes.
OX   NCBI_TaxID=83912;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed=11931040;
RA   Temeyer K.B., Soileau L.C., Pruett J.H.;
RT   "Cloning and sequence analysis of a cDNA encoding Pso o II, a mite
RT   group II allergen of the sheep scab mite (Acari: Psoroptidae).";
RL   J. Med. Entomol. 39:384-391(2002).
RN   [2]
RP   PARTIAL SEQUENCE OF N-TERMINUS.
RX   PubMed=10534947;
RA   Pruett J.H.;
RT   "Identification and purification of a 16-kDa allergen from Psoroptes
RT   ovis (Acarina: Psoroptidae).";
RL   J. Med. Entomol. 36:544-550(1999).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- ALLERGEN: Causes an allergic reaction in human. Common symptoms of
CC       mite allergy are bronchial asthma, allergic rhinitis and
CC       conjunctivitis.
CC   -!- SIMILARITY: Belongs to the NPC2 family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF187083; AAK61827.1; -.
DR   HSSP; Q00855; 1AHK.
DR   InterPro; IPR003172; E1_DerP2_DerF2.
DR   Pfam; PF02221; E1_DerP2_DerF2; 1.
DR   SMART; SM00737; ML; 1.
KW   Allergen; Direct protein sequencing; Signal.
FT   SIGNAL        1     17
FT   CHAIN        18    143       Mite group 2 allergen Pso o 2.
FT   DISULFID     25    134       By similarity.
FT   DISULFID     38     43       By similarity.
FT   DISULFID     89     94       By similarity.
SQ   SEQUENCE   143 AA;  15212 MW;  AF03533059DA838D CRC64;

  Query Match             39.4%;  Score 272.5;  DB 1;  Length 143;
  Best Local Similarity   37.5%;  Pred. No. 5.7e-19;
  Matches   48;  Conservative   35;  Mismatches   42;  Indels    3;  Gaps    3;

Qy          2 QVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDGL 61
              :|  :||   |:: : | || | : |:| :||    |     :||:||  |::| | |:|:
Db         19 KVKFQDCGKGEVESLEVEGCSG-DYCVIHKGKKLDLAISVTSNQDSANLKLDIVADINGV 77

Qy         62 SVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACAI 121
              ::|||:| : |||: ||:  || :|:|||:::| | | ::  ::  |::|| |:  | |
Db         78 QIEVPGVDHDGCHYVKCPIKKGQHFDVKYTYSIPAILPTTKAKII-AKIIGDKGLGGC-I 135

Qy        122 ATHAKIRD 129
                : :|:|
Db        136 VINGEIQD 143


RESULT 7
AL22_GLYDO
ID   AL22_GLYDO     STANDARD;      PRT;   125 AA.
AC   Q9NPQ4;
DT   05-JUL-2004 (Rel. 44, Created)
DT   05-JUL-2004 (Rel. 44, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Mite group 2 allergen Gly d 2.02.
OS   Glycyphagus domesticus (House itch mite).
```

```
OC   Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC   Acariformes; Sarcoptiformes; Astigmata; Glycyphagoidea; Glycyphagidae;
OC   Glycyphagus.
OX   NCBI_TaxID=105145;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE OF 1-18.
RX   MEDLINE=21135826; PubMed=11240953; DOI=10.1067/mai.2001.112264;
RA   Gafvelin G., Johansson E., Lundin A., Smith A.M., Chapman M.D.,
RA   Benjamin D.C., Derewenda U., van Hage-Hamsten M.;
RT   "Cross-reactivity studies of a new group 2 allergen from the dust mite
RT   Glycyphagus domesticus, Gly d 2, and group 2 allergens from
RT   Dermatophagoides pteronyssinus, Lepidoglyphus destructor, and
RT   Tyrophagus putrescentiae with recombinant allergens.";
RL   J. Allergy Clin. Immunol. 107:511-518(2001).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- ALLERGEN: Causes an allergic reaction in human. Common symptoms of
CC       mite allergy are bronchial asthma, allergic rhinitis and
CC       conjunctivitis.
CC   -!- SIMILARITY: Belongs to the NPC2 family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AJ272216; CAB76459.1; -.
DR   InterPro; IPR003172; E1_DerP2_DerF2.
DR   Pfam; PF02221; E1_DerP2_DerF2; 1.
DR   SMART; SM00737; ML; 1.
KW   Allergen; Direct protein sequencing.
SQ   SEQUENCE   125 AA;  13366 MW;  63607D3C6BF0AAE0 CRC64;

  Query Match             36.3%;  Score 251;  DB 1;  Length 125;
  Best Local Similarity   42.1%;  Pred. No. 6.5e-17;
  Matches   48;  Conservative   22;  Mismatches   42;  Indels    2;  Gaps    2;

Qy          6 KDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDGLSVDV 65
              |||    |: |: :  | | : |:| ||||  ||| | |||::  | |:: | : |  : |
Db          6 KDCGKGEVTELDITDCSG-DFCVIHRGKPLTLEAKFAANQDTTKATIKVLAKVAGTPIQV 64

Qy         66 PGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLAC 119
              ||:: : | :: ||:  |   | ||| || | |  :   || :::||:|||||
Db         65 PGLETDGCKFVKCPIKKGDPIDFKYTTTVPAILPKVK-AEVTAELVGDHGVLAC 117


RESULT 8
ALL2_TYRPU
ID   ALL2_TYRPU     STANDARD;      PRT;   141 AA.
AC   O02380;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Mite group 2 allergen Tyr p 2 precursor.
OS   Tyrophagus putrescentiae (Dust mite).
OC   Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC   Acariformes; Sarcoptiformes; Astigmata; Acaroidea; Acaridae;
OC   Tyrophagus.
OX   NCBI_TaxID=59818;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 16-22.
RX   MEDLINE=98151280; PubMed=9492316;
RA   Eriksson T.L.J., Johansson E., Whitley P., Schmidt M., Elsayed S.,
RA   van Hage-Hamsten M.;
RT   "Cloning and characterisation of a group II allergen from the dust
RT   mite Tyrophagus putrescentiae.";
RL   Eur. J. Biochem. 251:443-447(1998).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- ALLERGEN: Causes an allergic reaction in human. Common symptoms of
CC       mite allergy are bronchial asthma, allergic rhinitis and
CC       conjunctivitis.
CC   -!- SIMILARITY: Belongs to the NPC2 family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; Y12690; CAA73221.1; -.
DR   HSSP; Q00855; 1AHK.
DR   InterPro; IPR003172; E1_DerP2_DerF2.
DR   Pfam; PF02221; E1_DerP2_DerF2; 1.
DR   SMART; SM00737; ML; 1.
KW   Allergen; Direct protein sequencing; Signal.
FT   SIGNAL        1     15
FT   CHAIN        16    141       Mite group 2 allergen Tyr p 2.
FT   DISULFID     23    132       By similarity.
FT   DISULFID     36     41       By similarity.
FT   DISULFID     87     92       By similarity.
FT   CARBOHYD    103    103       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   141 AA;  14851 MW;  38EF9520010A04C1 CRC64;

  Query Match             35.6%;  Score 246.5;  DB 1;  Length 141;
  Best Local Similarity   39.8%;  Pred. No. 2.1e-16;
  Matches   51;  Conservative   25;  Mismatches   45;  Indels    7;  Gaps    4;

Qy          2 QVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDGL 61
              ||   ||   ||  | | || | : |:| : ||  : | | |||::   ::::   ::||
Db         17 QVKFTDCGKKEIASVAVDGCEG-DLCVIHKSKPVHVIAEFTANQDTCKIEVKVTGQLNGL 75

Qy         62 SVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVL--GDNGVLAC 119
              | :|||: : |  : |||  | :| : |: ||| : || : |   ||:|  |::|||||
Db         76 EVPIPGIETDGCKVLKCPLKKGTKYTMNYSVNVPSVVPNIKTV---VKLLATGEHGVLAC 132

Qy        120 -AIATHAK 126
               |: |  |
Db        133 GAVNTDVK 140


RESULT 9
AL21_GLYDO
ID   AL21_GLYDO     STANDARD;      PRT;   128 AA.
AC   Q9U5P7;
DT   05-JUL-2004 (Rel. 44, Created)
DT   05-JUL-2004 (Rel. 44, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Mite group 2 allergen Gly d 2.01.
OS   Glycyphagus domesticus (House itch mite).
OC   Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC   Acariformes; Sarcoptiformes; Astigmata; Glycyphagoidea; Glycyphagidae;
OC   Glycyphagus.
OX   NCBI_TaxID=105145;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE OF 1-18.
RX   MEDLINE=21135826; PubMed=11240953; DOI=10.1067/mai.2001.112264;
RA   Gafvelin G., Johansson E., Lundin A., Smith A.M., Chapman M.D.,
RA   Benjamin D.C., Derewenda U., van Hage-Hamsten M.;
RT   "Cross-reactivity studies of a new group 2 allergen from the dust mite
RT   Glycyphagus domesticus, Gly d 2, and group 2 allergens from
RT   Dermatophagoides pteronyssinus, Lepidoglyphus destructor, and
RT   Tyrophagus putrescentiae with recombinant allergens.";
RL   J. Allergy Clin. Immunol. 107:511-518(2001).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- ALLERGEN: Causes an allergic reaction in human. Common symptoms of
CC       mite allergy are bronchial asthma, allergic rhinitis and
CC       conjunctivitis.
CC   -!- SIMILARITY: Belongs to the NPC2 family.
CC   ---------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AJ249864; CAB59976.1; -.
DR   InterPro; IPR003172; E1_DerP2_DerF2.
DR   Pfam; PF02221; E1_DerP2_DerF2; 1.
DR   SMART; SM00737; ML; 1.
KW   Allergen; Direct protein sequencing.
SQ   SEQUENCE   128 AA;  13790 MW;  431A027FE89A7B03 CRC64;

  Query Match             35.1%;  Score 243;  DB 1;  Length 128;
  Best Local Similarity   39.7%;  Pred. No. 4.1e-16;
  Matches   48;  Conservative   32;  Mismatches   35;  Indels    6;  Gaps    4;

Qy          2 QVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG- 60
              :::  || ::|||| | | ||  |:| |||| |:| |:|||::|:  : : | |||
Db          2 KMNFTDCGHNEIKELSVSNCTGNY-CVIHRGKPLTLDAKFDANQDTASVGLVLTAIIDGD 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVK--VLGDNGVLA 118
              :::|:||:: ||| | ||:  |:  :: |  |: :|   :  :   ||  ::|::|||| 
Db         61 IAIDIPGLETNACKLMKCPIRKGEHQELIY--NIGEIPDATPEIKAKVKAQLIGEHGVLA 118

Qy        119 C 119
              |
Db        119 C 119


RESULT 10
ALL2_LEPDS
ID   ALL2_LEPDS     STANDARD;      PRT;   141 AA.
AC   P80384; Q8MYK7; Q8MYK8;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Mite group 2 allergen Lep d 2 precursor (Lep d 1) (Lep d I).
OS   Lepidoglyphus destructor (Fodder mite).
OC   Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC   Acariformes; Sarcoptiformes; Astigmata; Glycyphagoidea; Glycyphagidae;
OC   Lepidoglyphus.
OX   NCBI_TaxID=36936;
RN   [1]
RP   SEQUENCE FROM N.A. (LEP D 2.0101 AND LEP D 2.0201).
RX   MEDLINE=95377437; PubMed=7649288; DOI=10.1016/0014-5793(95)98164-E;
RA   Schmidt M., van der Ploeg I., Olsson S., van Hage-Hamsten M.;
RT   "cDNA analysis of the mite allergen Lep d 1 identifies two different
RT   isoallergens and variants.";
RL   FEBS Lett. 370:11-14(1995).
RN   [2]
RP   SEQUENCE FROM N.A. (LEP D 2.0103 AND LEP D 2.0203).
RA   Kaiser L., Rasool O., Gafvelin G., van Hage-Hamsten M., Johansson E.;
RT   "Lep d 2 polymorphisms in wild and cultured Lepidoglyphus mites.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 44-141 FROM N.A., AND SEQUENCE OF 17-140.
RX   MEDLINE=95010146; PubMed=7925475;
RA   Varela J., Ventas P., Carreira J., Barbas J.A., Gimenez-Gallego G.,
RA   Polo F.;
RT   "Primary structure of Lep d I, the main Lepidoglyphus destructor
RT   allergen.";
RL   Eur. J. Biochem. 225:93-98(1994).
RN   [4]
RP   PARTIAL SEQUENCE OF 17-45.
RA   Muthiah R., Miller M., Kagen S.;
RT   "Barn allergy: isolation and characterization of the major allergens
RT   of storagemites: L. destructor.";
RL   J. Allergy Clin. Immunol. 87:326-326(1991).
RN   [5]
RP   SEQUENCE OF 17-34.
RX   MEDLINE=92382323; PubMed=1355192; DOI=10.1016/0140-6736(92)92152-6;
RA   van Hage-Hamsten M., Bergman T., Johansson E., Persson B.,
RA   Joernvall H., Haerfast B., Johansson S.G.O.;
RT   "N-terminal aminoacid sequence of principal allergen of storage mite
RT   Lepidoglyphus destructor.";
RL   Lancet 340:614-614(1992).
CC   -!- SUBUNIT: Monomer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- POLYMORPHISM: The sequence shown is that of isoform Lep d 2.0101.
CC   -!- ALLERGEN: Causes an allergic reaction in human. Common symptoms of
CC       mite allergy are bronchial asthma, allergic rhinitis and
CC       conjunctivitis.
CC   -!- SIMILARITY: Belongs to the NPC2 family.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; X83875; CAA58755.1; -.
DR   EMBL; X83876; CAA58756.1; -.
DR   EMBL; X89014; CAA61419.1; -.
DR   EMBL; AJ487972; CAD32313.1; -.
DR   EMBL; AJ487973; CAD32314.1; -.
DR   EMBL; X81399; CAA57160.1; -.
DR   PIR; S66500; S66500.
DR   HSSP; Q00855; 1AHK.
DR   InterPro; IPR003172; E1_DerP2_DerF2.
DR   Pfam; PF02221; E1_DerP2_DerF2; 1.
DR   SMART; SM00737; ML; 1.
KW   Allergen; Direct protein sequencing; Polymorphism; Repeat; Signal.
FT   SIGNAL       1    16
FT   CHAIN       17   141       Mite group 2 allergen Lep d 2.
FT   DOMAIN      64    73       3 X 2 AA repeats of K-V.
FT   REPEAT      64    65       1.
FT   REPEAT      68    69       2.
FT   REPEAT      72    73       3.
FT   DISULFID    24   133       By similarity.
FT   DISULFID    37    42       By similarity.
FT   DISULFID    88    93       By similarity.
FT   VARIANT     35    35       T -> S (in Lep d 2.0201 and Lep d
FT                              2.0203).
FT   VARIANT     48    48       E -> Q (in Lep d 2.0201 and Lep d
FT                              2.0203).
FT   VARIANT     53    53       E -> D (in Lep d 2.0201 and Lep d
FT                              2.0203).
FT   VARIANT     63    63       A -> N (in Lep d 2.0201 and Lep d
FT                              2.0203).
FT   VARIANT     71    71       A -> T (in Lep d 2.0103).
FT   VARIANT     90    90       F -> V (in Lep d 2.0201 and Lep d
FT                              2.0203).
FT   VARIANT     91    91       I -> L (in Lep d 2.0201 and Lep d
FT                              2.0203).
FT   VARIANT     95    95       V -> I (in Lep d 2.0201 and Lep d
FT                              2.0203).
FT   VARIANT    104   104       I -> N (in Lep d 2.0201 and Lep d
FT                              2.0203).
FT   VARIANT    106   106       S -> G (in Lep d 2.0201 and Lep d
FT                              2.0203).
FT   VARIANT    107   107       G -> M (in Lep d 2.0201 and Lep d
FT                              2.0203).
FT   VARIANT    116   116       V -> I (in Lep d 2.0201 and Lep d
FT                              2.0203).
FT   VARIANT    118   118       A -> V (in Lep d 2.0203).
FT   VARIANT    125   125       I -> V (in Lep d 2.0201 and Lep d
FT                              2.0203).
FT   VARIANT    136   136       V -> I (in Lep d 2.0201 and Lep d
FT                              2.0203).
FT   CONFLICT    26    26       H -> K (in Ref. 5).
FT   CONFLICT    30    30       T -> K (in Ref. 5).
SQ   SEQUENCE   141 AA;  14773 MW;  9AC96F74D6826FA4 CRC64;

  Query Match             34.8%;  Score 240.5;  DB 1;  Length 141;
```

```
  Best Local Similarity   36.1%;  Pred. No. 8.1e-16;
  Matches   44;  Conservative   31;  Mismatches   44;  Indels    3;  Gaps    3;

Qy          6 KDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDGLSVDV 65
              ||| : |: |: : || | : |:| ||:    ||| | |||::|   |:: | : | :: |
Db         22 KDCGHGEVTELDITGCSG-DTCVIHRGEKMTLEAKFAANQDTAKVTIKVLAKVAGTTIQV 80

Qy         66 PGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACAIATHA 125
              ||:: : | :: ||:  |:  |  |:  :| | |  :   || :::||:||:||    |
Db         81 PGLETDGCKFIKCPVKKGEALDFIYSGTIPAITPKVK-ADVTAELIGDHGVMACG-TVHG 138

Qy        126 KI 127
              ::
Db        139 QV 140


RESULT 11
Q7QCX5
ID   Q7QCX5      PRELIMINARY;      PRT;   163 AA.
AC   Q7QCX5;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   AgCP1115 (Fragment).
GN   Name=agCG51964; ORFNames=ENSANGG00000014522;
OS   Anopheles gambiae str. PEST.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX   NCBI_TaxID=180454;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PEST;
RA   Anopheles Genome Sequencing Consortium;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- CAUTION: The sequence shown here is derived from an
CC       EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC       preliminary data.
DR   EMBL; AAAB01008859; EAA07711.1; -.
DR   InterPro; IPR003172; E1_DerP2_DerF2.
DR   Pfam; PF02221; E1_DerP2_DerF2; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   163 AA;  17196 MW;  4EAC6C34DD21C04F CRC64;

  Query Match             17.7%;  Score 122.5;  DB 2;  Length 163;
  Best Local Similarity   30.2%;  Pred. No. 0.00043;
  Matches   39;  Conservative   22;  Mismatches   57;  Indels   11;  Gaps    7;

Qy          3 VDVKDCANHE--IKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              :::  |:|:    :|| |||| : || :     |     |     : |  ::::||: |
Db         34 LEIIQCSNNRPTPQEVTVPGC-TSLPCQVPNQSDFNFSVRFAPTFPTNTLTVDVRASLLG 92

Qy         61 LSV--DVPGIDPNACHYMN--CPLVNGQQYDIKYTWNVPKIAP-NSENVVVTVKVLGDNG 115
              | :  :||    | |: :|  |||  ||   :  |   |  ||     | :  :: || |
Db         93 LFLPYEVPEHLRNGCNNINTSCPLTAGQ--SVTLTGTAPVEAPLTGVTVTMEFEITGDGG 150

Qy        116 -VLACAIAT 123
               |  |  ||
Db        151 QVAVCFAAT 159


RESULT 12
Q66K95
ID   Q66K95      PRELIMINARY;      PRT;   151 AA.
AC   Q66K95;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein.
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8364;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RA   Klein S., Gerhard D.S.;
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC080500; AAH80500.1; -.
DR   InterPro; IPR003172; E1_DerP2_DerF2.
DR   Pfam; PF02221; E1_DerP2_DerF2; 1.
DR   SMART; SM00737; ML; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   151 AA;  16209 MW;  781FE93CEC4D2D80 CRC64;

  Query Match             16.9%;  Score 117;  DB 2;  Length 151;
  Best Local Similarity   33.3%;  Pred. No. 0.0014;
  Matches   31;  Conservative   16;  Mismatches   40;  Indels    6;  Gaps    4;

Qy          6 KDCANHEIKEVL--VPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDGLSV 63
              ||| :   | |   |  |   ||| : ||  : : | | :| || :|   :   | |::|
Db         26 KDCGSQSGKLVTLDVSPC-PEEPCPLVRGSTYTVNATFVSNVNSKSASAVVHGIIAGIAV 84

Qy         64 DVPGIDPNACHY-MNCPLVNGQQYDIKYTWNVP 95
                |  :|: |   ::||: :|| |   |   :|
Db         85 PFPISEPDGCKSGISCPINSGQTY--TYVTKLP 115


RESULT 13
NPC2_PIG
ID   NPC2_PIG       STANDARD;      PRT;   149 AA.
AC   O97763;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Epididymal secretory protein E1 precursor (Niemann Pick type C2
DE   protein homolog) (16 kDa secretory protein).
GN   Name=NPC2;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 20-39.
RC   TISSUE=Epididymis;
RX   PubMed=10366780; DOI=10.1016/S1388-1981(99)00070-0;
RA   Okamura N., Kiuchi S., Tamba M., Kashima T., Hiramoto S., Baba T.,
RA   Dacheux F., Dacheux J.-L., Sugita Y., Jin Y.-Z.;
RT   "A porcine homolog of the major secretory protein of human epididymis,
RT   HE1, specifically binds cholesterol.";
RL   Biochim. Biophys. Acta 1438:377-387(1999).
CC   -!- FUNCTION: May be involved in the regulation of the lipid
```

```
CC       composition of sperm membranes during the maturation in the
CC       epididymis. Binds cholesterol in a 1:1 ratio.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Found in the fluid from the distal caput to
CC       cauda epididymis, not detected in the rete testis and the proximal
CC       and middle caput epididymal fluids.
CC   -!- PTM: N-glycosylated. Found in the epididymal fluid as a 19 kDa
CC       glycoprotein that is processed during its passage through the
CC       epididymis into a 16 kDa protein.
CC   -!- SIMILARITY: Belongs to the NPC2 family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U62253; AAD00096.1; -.
DR   HSSP; P79345; 1NEP.
DR   InterPro; IPR003172; E1_DerP2_DerF2.
DR   Pfam; PF02221; E1_DerP2_DerF2; 1.
DR   SMART; SM00737; ML; 1.
KW   Direct protein sequencing; Glycoprotein; Signal.
FT   SIGNAL        1     19
FT   CHAIN        20    149       Epididymal secretory protein E1.
FT   DISULFID     27    140       By similarity.
FT   DISULFID     42     47       By similarity.
FT   DISULFID     93     99       By similarity.
FT   CARBOHYD     58     58       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   149 AA;  16288 MW;  78F0920057CA0102 CRC64;

  Query Match             16.7%;  Score 115.5;  DB 1;  Length 149;
  Best Local Similarity   29.7%;  Pred. No. 0.0019;
  Matches   35;  Conservative   21;  Mismatches   55;  Indels    7;  Gaps    5;

Qy          1 DQVDVKDCAN--HEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASI 58
              :  :|| :    ||||  |  |   :|| : :|: : :   | :|  |  :|  :   :
Db         20 EPVHFRDCGSGVGVIKEVNVNPC-PTQPCQLHKGQSYSVNVTFTSNTQSKGSKAVVHGIV 78

Qy         59 DGLSVDVPGIDPNACHY-MNCPLVNGQQYDIKYTWNVP-KIAPNSENVVVTVKVLGDN 114
               |: :  |  ||: |   :|||:   | |   |   :| |    |  :||  |:  ||
Db         79 MGVPIPFPIPDPDGCKSGINCPIQKDQTY--SYLNKLPVKAEYPSIKLVVEWKLQDDN 134


RESULT 14
NPC2_HUMAN
ID   NPC2_HUMAN     STANDARD;      PRT;   151 AA.
AC   P61916; Q15668; Q29413;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Epididymal secretory protein E1 precursor (Niemann-Pick disease type
DE   C2 protein) (hE1).
GN   Name=NPC2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Epididymis;
RX   MEDLINE=93119659; PubMed=8418812;
RA   Krull N., Ivell R., Osterhoff C., Kirchhoff C.;
RT   "Region-specific variation of gene expression in the human epididymis
RT   as revealed by in situ hybridization with tissue-specific cDNAs.";
RL   Mol. Reprod. Dev. 34:16-24(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [3]
RP   DISEASE.
RX   MEDLINE=20574615; PubMed=11125141; DOI=10.1126/science.290.5500.2298;
RA   Naureckiene S., Sleat D.E., Lackland H., Fensom A., Vanier M.T.,
RA   Wattiaux R., Jadot M., Lobel P.;
RT   "Identification of HE1 as the second gene of Niemann-Pick C disease.";
RL   Science 290:2298-2301(2000).
RN   [4]
RP   VARIANT NP-C2 SER-67.
RX   MEDLINE=21473745; PubMed=11567215;
RA   Millat G., Chikh K., Naureckiene S., Sleat D.E., Fensom A.H.,
RA   Higaki K., Elleder M., Lobel P., Vanier M.T.;
RT   "Niemann-Pick disease type C: spectrum of HE1 mutations and
RT   genotype/phenotype correlations in the NPC2 group.";
RL   Am. J. Hum. Genet. 69:1013-1021(2001).
RN   [5]
RP   VARIANT NP-C2 MET-39.
RX   MEDLINE=22334746; PubMed=12447927; DOI=10.1002/ana.10366;
RA   Klunemann H.H., Elleder M., Kaminski W.E., Snow K., Peyser J.M.,
RA   O'Brien J.F., Munoz D., Schmitz G., Klein H.E., Pendlebury W.W.;
RT   "Frontal lobe atrophy due to a mutation in the cholesterol binding
RT   protein HE1/NPC2.";
RL   Ann. Neurol. 52:743-749(2002).
CC   -!- FUNCTION: May be involved in the regulation of the lipid
CC       composition of sperm membranes during the maturation in the
CC       epididymis (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- TISSUE SPECIFICITY: Epididymis.
CC   -!- DISEASE: Defects in NPC2 are the cause of Niemann-Pick disease
CC       type C2 (NP-C2) [MIM:607625], a fatal autosomal recessive
CC       hereditary disease characterized by the accumulation of low-
CC       density lipoprotein-derived cholesterol in lysosomes.
CC   -!- SIMILARITY: Belongs to the NPC2 family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X67698; CAA47928.1; -.
DR   EMBL; BC002532; AAH02532.1; -.
DR   EMBL; A18921; CAA01431.1; -.
DR   PIR; I38365; I38365.
DR   HSSP; P79345; 1NEP.
DR   Genew; HGNC:14537; NPC2.
DR   MIM; 601015; -.
DR   MIM; 607625; -.
DR   InterPro; IPR003172; E1_DerP2_DerF2.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF02221; E1_DerP2_DerF2; 1.
DR   SMART; SM00737; ML; 1.
```

```
KW   Glycoprotein; Polymorphism; Signal.
FT   SIGNAL        1     19       Potential.
FT   CHAIN        20    151       Epididymal secretory protein E1.
FT   DISULFID     27    140       By similarity.
FT   DISULFID     42     47       By similarity.
FT   DISULFID     93     99       By similarity.
FT   CARBOHYD     58     58       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    135    135       N-linked (GlcNAc. . .) (Potential).
FT   VARIANT      39     39       V -> M (in NP-C2).
FT                                /FTId=VAR_015848.
FT   VARIANT      67     67       S -> P (in NP-C2; dbSNP:11694).
FT                                /FTId=VAR_015849.
FT   VARIANT      86     86       P -> L (in dbSNP:4688).
FT                                /FTId=VAR_011899.
SQ   SEQUENCE   151 AA;  16570 MW;  B141B611805DC910 CRC64;

  Query Match             16.2%;  Score 112;  DB 1;  Length 151;
  Best Local Similarity   29.1%;  Pred. No. 0.0042;
  Matches   37;  Conservative   26;  Mismatches   50;  Indels   14;  Gaps    7;

Qy          1 DQVDVKDCANHE--IKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASI 58
              : |  ||| : :  |||| |  |   :|| : :|: : :   | :|  | ::|  :   :
Db         20 EPVQFKDCGSVDGVIKEVNVSPC-PTQPCQLSKGQSYSVNVTFTSNIQSKSSKAVVHGIL 78

Qy         59 DGLSVDVPGIDPNACHY-MNCPLVNGQQYDIKYTWNVPKIAPNSE----NVVVTVKVLGD 113
              |: |  |  :|: |   :|||:    | |  |:: : |:   ||     :||  ::  |
Db         79 MGVPVPFPIPEPDGCKSGINCPI----QKDKTYSY-LNKLPVKSEYPSIKLVVEWQLQDD 133

Qy        114 -NGVLAC 119
               | | |
Db        134 KNQSLFC 140


RESULT 15
NPC2_MACFA
ID   NPC2_MACFA     STANDARD;      PRT;   151 AA.
AC   P61918; Q15668; Q29413;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Epididymal secretory protein E1 precursor (Niemann Pick type C2
DE   protein homolog) (Epididymal secretory protein 14.6) (ESP14.6).
GN   Name=NPC2;
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Epididymis;
RX   MEDLINE=95180740; PubMed=7875608; DOI=10.1016/0378-1119(94)00739-F;
RA   Perry A.C.F., Jones R., Hall L.;
RT   "The monkey ESP14.6 mRNA, a novel transcript expressed at high levels
RT   in the epididymis.";
RL   Gene 153:291-292(1995).
CC   -!- FUNCTION: May be involved in the regulation of the lipid
CC       composition of sperm membranes during the maturation in the
CC       epididymis (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC   -!- TISSUE SPECIFICITY: Epididymis.
CC   -!- SIMILARITY: Belongs to the NPC2 family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X78134; CAA55013.1; -.
DR   PIR; I53929; I53929.
DR   HSSP; P79345; 1NEP.
DR   InterPro; IPR003172; E1_DerP2_DerF2.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF02221; E1_DerP2_DerF2; 1.
DR   SMART; SM00737; ML; 1.
KW   Glycoprotein; Signal.
FT   SIGNAL        1     19       Potential.
FT   CHAIN        20    151       Epididymal secretory protein E1.
FT   DISULFID     27    140       By similarity.
FT   DISULFID     42     47       By similarity.
FT   DISULFID     93     99       By similarity.
FT   CARBOHYD     58     58       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    135    135       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   151 AA;  16570 MW;  B141B611805DC910 CRC64;

  Query Match             16.2%;  Score 112;  DB 1;  Length 151;
  Best Local Similarity   29.1%;  Pred. No. 0.0042;
  Matches   37;  Conservative   26;  Mismatches   50;  Indels   14;  Gaps    7;

Qy          1 DQVDVKDCANHE--IKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASI 58
              : |  ||| : :  |||| |  |   :|| : :|: : :   | :|  | ::|  :   :
Db         20 EPVQFKDCGSVDGVIKEVNVSPC-PTQPCQLSKGQSYSVNVTFTSNIQSKSSKAVVHGIL 78

Qy         59 DGLSVDVPGIDPNACHY-MNCPLVNGQQYDIKYTWNVPKIAPNSE----NVVVTVKVLGD 113
              |: |  |  :|: |   :|||:    | |  |:: : |:   ||     :||  ::  |
Db         79 MGVPVPFPIPEPDGCKSGINCPI----QKDKTYSY-LNKLPVKSEYPSIKLVVEWQLQDD 133

Qy        114 -NGVLAC 119
               | | |
Db        134 KNQSLFC 140


Search completed: September  9, 2005, 15:23:02
Job time : 82 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 9, 2005, 15:06:59 ; Search time 27 Seconds
(without alignments)
356.657 Million cell updates/sec

Title: US-10-001-245C-36
Perfect score: 692
Sequence: 1 DQVDVKDCANHEIKEVLVPG.....VLGDNGVLACAIATHAKIRD 129

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	638	92.2	145	4	US-09-949-889-3	Sequence 3, Appli
2	635	91.8	145	3	US-08-460-040-6	Sequence 6, Appli
3	635	91.8	146	1	US-07-945-288-4	Sequence 4, Appli
4	635	91.8	146	1	US-08-462-831-4	Sequence 4, Appli
5	635	91.8	146	1	US-08-461-809-4	Sequence 4, Appli
6	635	91.8	146	1	US-08-461-441-4	Sequence 4, Appli
7	635	91.8	146	2	US-08-482-142-4	Sequence 4, Appli
8	635	91.8	146	2	US-08-478-572-4	Sequence 4, Appli
9	635	91.8	146	3	US-08-484-296-4	Sequence 4, Appli
10	635	91.8	146	5	PCT-US93-08518-4	Sequence 4, Appli
11	627	90.6	129	1	US-08-462-831-12	Sequence 12, Appl
12	627	90.6	129	1	US-08-461-809-12	Sequence 12, Appl
13	627	90.6	129	1	US-08-461-441-12	Sequence 12, Appl
14	627	90.6	129	5	PCT-US93-08518-12	Sequence 12, Appl
15	622	89.9	129	1	US-07-945-288-12	Sequence 12, Appl
16	621	89.7	129	4	US-09-949-889-4	Sequence 4, Appli
17	603	87.1	129	2	US-08-482-142-157	Sequence 157, App
18	603	87.1	129	2	US-08-478-572-157	Sequence 157, App
19	603	87.1	129	3	US-08-484-296-157	Sequence 157, App
20	596	86.1	129	2	US-08-482-142-159	Sequence 159, App
21	596	86.1	129	2	US-08-478-572-159	Sequence 159, App
22	596	86.1	129	3	US-08-484-296-159	Sequence 159, App
23	592	85.5	129	3	US-08-930-264-4	Sequence 4, Appli
24	590.5	85.3	130	2	US-08-482-142-158	Sequence 158, App
25	590.5	85.3	130	2	US-08-478-572-158	Sequence 158, App
26	590.5	85.3	130	3	US-08-484-296-158	Sequence 158, App
27	590	85.3	129	3	US-08-930-264-6	Sequence 6, Appli
28	590	85.3	129	3	US-08-930-264-16	Sequence 16, Appl
29	590	85.3	129	3	US-08-930-264-20	Sequence 20, Appl
30	590	85.3	142	1	US-08-288-888-4	Sequence 4, Appli
31	590	85.3	142	2	US-08-910-075-4	Sequence 4, Appli
32	590	85.3	142	2	US-08-905-801A-4	Sequence 4, Appli
33	589	85.1	129	3	US-08-930-264-18	Sequence 18, Appl
34	588	85.0	129	3	US-08-930-264-2	Sequence 2, Appli
35	588	85.0	142	1	US-08-288-888-2	Sequence 2, Appli
36	588	85.0	142	2	US-08-910-075-2	Sequence 2, Appli
37	588	85.0	142	2	US-08-905-801A-2	Sequence 2, Appli
38	587	84.8	129	3	US-08-930-264-24	Sequence 24, Appl
39	586	84.7	129	3	US-08-930-264-8	Sequence 8, Appli
40	585	84.5	129	1	US-07-945-288-8	Sequence 8, Appli
41	585	84.5	129	1	US-08-462-831-8	Sequence 8, Appli
42	585	84.5	129	1	US-08-461-809-8	Sequence 8, Appli
43	585	84.5	129	1	US-08-461-441-8	Sequence 8, Appli
44	585	84.5	129	2	US-08-482-142-8	Sequence 8, Appli
45	585	84.5	129	2	US-08-478-572-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-949-889-3
; Sequence 3, Application US/09949889
; Patent No. 6800290
; GENERAL INFORMATION:
; APPLICANT: CONSIGLIO NAZIONALE DELLE RICERCHE
; TITLE OF INVENTION: VARIANTS OF ALLERGENIC PROTEINS OF THE GROUP 2 OF
; TITLE OF INVENTION: DERMATOPHAGOIDES
; FILE REFERENCE: Cons Naz Ric
; CURRENT APPLICATION NUMBER: US/09/949,889
; CURRENT FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-09-949-889-3

Query Match 92.2%; Score 638; DB 4; Length 145;
Best Local Similarity 91.5%; Pred. No. 2.1e-67;
Matches 118; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||:||||||||:||||| |||||||||:|||||||| ||||||||||||
Db         17 DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNSKTAKIEIKASIDG 76

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | |||||||||||||| |||| |||||||||||||||| ||||||||||:||:||||||
Db         77 LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVMGDDGVLACA 136

Qy        121 IATHAKIRD 129
              |||||||||
Db        137 IATHAKIRD 145
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RESULT 2
US-08-460-040-6
; Sequence 6, Application US/08460040
; Patent No. 6071522
; GENERAL INFORMATION:
; APPLICANT: Thomas, Wayne R.
; TITLE OF INVENTION: Cloning of Mite Allergens
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA

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;       ZIP:  02109-1875
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/460,040
;       FILING DATE:  2-JUNE-95
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/162,722
;       FILING DATE:  8-NOV-93
;       APPLICATION NUMBER:  07/458,642
;       FILING DATE:  13-FEB-90
;       APPLICATION NUMBER:  PCT/AU88/00195
;       FILING DATE:  17-JUNE-88
;       APPLICATION NUMBER:  PI 2523/87
;       FILING DATE:  18-JUNE-87
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Amy E. Mandragouras
;       REGISTRATION NUMBER:  36,207
;       REFERENCE/DOCKET NUMBER:  IMI-021CN2
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617)227-7400
;       TELEFAX:  (617)227-5941
;   INFORMATION FOR SEQ ID NO:  6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  145 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-460-040-6

  Query Match             91.8%;  Score 635;  DB 3;  Length 145;
  Best Local Similarity   90.7%;  Pred. No. 4.7e-67;
  Matches  117;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              |||||||||||||||:||||||||:||||| |||||||||:||||||: ||||||||||||
Db         17 DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNTKTAKIEIKASIDG 76

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | ||||||||||||| |||| |||||||||||||||| ||||||||||:||:||||||
Db         77 LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVMGDDGVLACA 136

Qy        121 IATHAKIRD 129
              |||||||||
Db        137 IATHAKIRD 145


RESULT 3
US-07-945-288-4
; Sequence 4, Application US/07945288
; Patent No. 5433948
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Wayne R.
;    APPLICANT:  Chua, Kaw-Yan
;    TITLE OF INVENTION:  CLONING AND SEQUENCING OF ALLERGENS FROM
;    TITLE OF INVENTION:  DERMATOPHAGOIDES (HOUSE DUST MITES)
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 STATE STREET, SUITE 510
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII TEXT
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/945,288
;      FILING DATE:  19920910
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  580,655
;      FILING DATE:  11 SEPTEMBER 1990
;      APPLICATION NUMBER:  458,642
;      FILING DATE:  13 FEBRUARY 1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MANDRAGOURAS, AMY E.
;      REGISTRATION NUMBER:  P36,207
;      REFERENCE/DOCKET NUMBER:  IPC-010CC (IMI-024)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  146 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-945-288-4

  Query Match             91.8%;  Score 635;  DB 1;  Length 146;
  Best Local Similarity   90.7%;  Pred. No. 4.7e-67;
  Matches  117;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              |||||||||||||||:||||||||:||||| |||||||||:||||||: ||||||||||||
Db         18 DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNTKTAKIEIKASIDG 77

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | ||||||||||||| |||| |||||||||||||||| ||||||||||:||:||||||
Db         78 LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVMGDDGVLACA 137

Qy        121 IATHAKIRD 129
              |||||||||
Db        138 IATHAKIRD 146


RESULT 4
US-08-462-831-4
; Sequence 4, Application US/08462831
; Patent No. 5552142
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  T CELL EPITOPES OF THE MAJOR ALLERGENS FROM
;    TITLE OF INVENTION:  DERMATOPHAGOIDES
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 STATE STREET, SUITE 510
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII TEXT
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/462,831
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/945,288
;      FILING DATE:  10 SEPTEMBER 1992
;      APPLICATION NUMBER:  US 580,655
;      FILING DATE:  11 SEPTEMBER 1990
;      APPLICATION NUMBER:  US 458,642
;      FILING DATE:  13 FEBRUARY 1990
```

```
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MANDRAGOURAS, AMY E.
;      REGISTRATION NUMBER:  36,207
;      REFERENCE/DOCKET NUMBER:  IPC-010CC (IMI-024)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  146 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-462-831-4

  Query Match             91.8%;  Score 635;  DB 1;  Length 146;
  Best Local Similarity   90.7%;  Pred. No. 4.7e-67;
  Matches  117;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||:||||||||:||||| |||||||||:||||||: ||||||||||||
Db         18 DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNTKTAKIEIKASIDG 77

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | ||||||||||||| |||| |||||||||||||||| ||||||||||:||:||||||
Db         78 LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVMGDDGVLACA 137

Qy        121 IATHAKIRD 129
              |||||||||
Db        138 IATHAKIRD 146


RESULT 5
US-08-461-809-4
; Sequence 4, Application US/08461809
; Patent No. 5770202
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  T CELL EPITOPES OF THE MAJOR ALLERGENS FROM
;    TITLE OF INVENTION:  DERMATOPHAGOIDES
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 STATE STREET, SUITE 510
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII TEXT
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/461,809
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/945,288
;      FILING DATE:  10 SEPTEMBER 1992
;      APPLICATION NUMBER:  US 580,655
;      FILING DATE:  11 SEPTEMBER 1990
;      APPLICATION NUMBER:  US 458,642
;      FILING DATE:  13 FEBRUARY 1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MANDRAGOURAS, AMY E.
;      REGISTRATION NUMBER:  36,207
;      REFERENCE/DOCKET NUMBER:  IPC-010CC (IMI-024)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  146 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-461-809-4

  Query Match             91.8%;  Score 635;  DB 1;  Length 146;
  Best Local Similarity   90.7%;  Pred. No. 4.7e-67;
  Matches  117;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||:||||||||:||||| |||||||||:||||||: ||||||||||||
Db         18 DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNTKTAKIEIKASIDG 77

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | ||||||||||||| |||| |||||||||||||||| ||||||||||:||:||||||
Db         78 LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVMGDDGVLACA 137

Qy        121 IATHAKIRD 129
              |||||||||
Db        138 IATHAKIRD 146


RESULT 6
US-08-461-441-4
; Sequence 4, Application US/08461441
; Patent No. 5773002
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  T CELL EPITOPES OF THE MAJOR ALLERGENS FROM
;    TITLE OF INVENTION:  DERMATOPHAGOIDES
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 STATE STREET, SUITE 510
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII TEXT
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/461,441
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/945,288
;      FILING DATE:  10 SEPTEMBER 1992
;      APPLICATION NUMBER:  US 580,655
;      FILING DATE:  11 SEPTEMBER 1990
;      APPLICATION NUMBER:  US 458,642
;      FILING DATE:  13 FEBRUARY 1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MANDRAGOURAS, AMY E.
;      REGISTRATION NUMBER:  36,207
;      REFERENCE/DOCKET NUMBER:  IPC-010CC (IMI-024)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  146 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-461-441-4

  Query Match             91.8%;  Score 635;  DB 1;  Length 146;
  Best Local Similarity   90.7%;  Pred. No. 4.7e-67;
  Matches  117;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;
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Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||:||||||||:||||| |||||||||:||||||: ||||||||||||
Db         18 DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNTKTAKIEIKASIDG 77

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | |||||||||||||| |||| |||||||||||||||| ||||||||||:||:||||||
Db         78 LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVMGDDGVLACA 137

Qy        121 IATHAKIRD 129
              |||||||||
Db        138 IATHAKIRD 146
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RESULT 7
US-08-482-142-4
; Sequence 4, Application US/08482142
; Patent No. 5820862
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Franzen, Henry
; APPLICANT: Chen, Xian
; APPLICANT: Evans, Sean
; APPLICANT: Shaked, Ze'ev
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,142
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/445,307
; FILING DATE: 07 June 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAIG, ANNE I.
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 017.6US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-482-142-4

Query Match 91.8%; Score 635; DB 2; Length 146;
Best Local Similarity 90.7%; Pred. No. 4.7e-67;
Matches 117; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||:||||||||:||||| |||||||||:||||||: ||||||||||||
Db         18 DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNTKTAKIEIKASIDG 77

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | |||||||||||||| |||| |||||||||||||||| ||||||||||:||:||||||
Db         78 LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVMGDDGVLACA 137

Qy        121 IATHAKIRD 129
              |||||||||
Db        138 IATHAKIRD 146
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RESULT 8
US-08-478-572-4
; Sequence 4, Application US/08478572
; Patent No. 5968526
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Franzen, Henry
; APPLICANT: Chen, Xian
; APPLICANT: Evans, Sean
; APPLICANT: Shaked, Ze'ev
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,572
; FILING DATE: 07-June-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/445,307
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAIG, ANNE I.
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 017.6US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-478-572-4

Query Match 91.8%; Score 635; DB 2; Length 146;
Best Local Similarity 90.7%; Pred. No. 4.7e-67;
Matches 117; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||:||||||||:||||| |||||||||:||||||: ||||||||||||
Db         18 DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNTKTAKIEIKASIDG 77

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | |||||||||||||| |||| |||||||||||||||| ||||||||||:||:||||||
Db         78 LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVMGDDGVLACA 137

Qy        121 IATHAKIRD 129
              |||||||||
Db        138 IATHAKIRD 146
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RESULT 9
US-08-484-296-4
; Sequence 4, Application US/08484296
; Patent No. 6268491
;  GENERAL INFORMATION:
;    APPLICANT:  Garman, Richard
;    APPLICANT:  Greenstein, Julia
;    APPLICANT:  Kuo, Mei-chang
;    APPLICANT:  Rogers, Bruce
;    APPLICANT:  Franzen, Henry
;    APPLICANT:  Chen, Xian
;    APPLICANT:  Evans, Sean
;    APPLICANT:  Shaked, Ze'ev
;    TITLE OF INVENTION:  T CELL EPITOPES OF THE MAJOR ALLERGENS
;    TITLE OF INVENTION:  FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
;    NUMBER OF SEQUENCES:  207
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  IMMULOGIC PHARMACEUTICAL CORPORATION
;      STREET:  610 LINCOLN STREET
;      CITY:  WALTHAM
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII TEXT
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/484,296
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/445,307
;      FILING DATE:  07 June 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  CRAIG, ANNE I.
;      REGISTRATION NUMBER:  32,976
;      REFERENCE/DOCKET NUMBER:  017.6US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 466-6000
;      TELEFAX:  (617) 466-6040
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  146 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-484-296-4

  Query Match             91.8%;  Score 635;  DB 3;  Length 146;
  Best Local Similarity   90.7%;  Pred. No. 4.7e-67;
  Matches  117;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||:||||||||:||||| |||||||||:||||||: ||||||||||||
Db         18 DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNTKTAKIEIKASIDG 77

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | ||||||||||||| |||| |||||||||||||||| ||||||||||:||:||||||
Db         78 LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVMGDDGVLACA 137

Qy        121 IATHAKIRD 129
              |||||||||
Db        138 IATHAKIRD 146


RESULT 10
PCT-US93-08518-4
; Sequence 4, Application PC/TUS9308518
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  T CELL EPITOPES OF THE MAJOR ALLERGENS FROM
;    TITLE OF INVENTION:  DERMATOPHAGOIDES
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 STATE STREET, SUITE 510
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII TEXT
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/08518
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/945,288
;      FILING DATE:  10 SEPTEMBER 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MANDRAGOURAS, AMY E.
;      REGISTRATION NUMBER:  36,207
;      REFERENCE/DOCKET NUMBER:  IPC-010CC (IMI-024)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  146 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US93-08518-4

  Query Match             91.8%;  Score 635;  DB 5;  Length 146;
  Best Local Similarity   90.7%;  Pred. No. 4.7e-67;
  Matches  117;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||:||||||||:||||| |||||||||:||||||: ||||||||||||
Db         18 DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNTKTAKIEIKASIDG 77

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | ||||||||||||| |||| |||||||||||||||| ||||||||||:||:||||||
Db         78 LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVMGDDGVLACA 137

Qy        121 IATHAKIRD 129
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Db        138 IATHAKIRD 146


RESULT 11
US-08-462-831-12
; Sequence 12, Application US/08462831
; Patent No. 5552142
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  T CELL EPITOPES OF THE MAJOR ALLERGENS FROM
;    TITLE OF INVENTION:  DERMATOPHAGOIDES
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 STATE STREET, SUITE 510
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII TEXT
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/462,831
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/945,288
;      FILING DATE:  10 SEPTEMBER 1992
;      APPLICATION NUMBER:  US 580,655
;      FILING DATE:  11 SEPTEMBER 1990
;      APPLICATION NUMBER:  US 458,642
;      FILING DATE:  13 FEBRUARY 1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MANDRAGOURAS, AMY E.
;      REGISTRATION NUMBER:  36,207
;      REFERENCE/DOCKET NUMBER:  IPC-010CC (IMI-024)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  129 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc feature
;      LOCATION:  47
;      OTHER INFORMATION:  /label=Xaa is Thr or Ser
;    FEATURE:
;      NAME/KEY:  misc feature
;      LOCATION:  114
;      OTHER INFORMATION:  /label=Xaa is Asp or Asn
;    FEATURE:
;      NAME/KEY:  misc feature
;      LOCATION:  127
;      OTHER INFORMATION:  /label=Xaa is Ile or Leu
US-08-462-831-12

  Query Match             90.6%;  Score 627;  DB 1;  Length 129;
  Best Local Similarity   89.9%;  Pred. No. 3.5e-66;
  Matches  116;  Conservative    4;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||:||||||||:||||| |||||||||:||||||  ||||||||||||
Db          1 DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNXKTAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | |||||||||||||| |||| |||||||||||||||| ||||||||||:|| ||||||
Db         61 LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVMGDXGVLACA 120

Qy        121 IATHAKIRD 129
              ||||||  ||
Db        121 IATHAKXRD 129


RESULT 12
US-08-461-809-12
; Sequence 12, Application US/08461809
; Patent No. 5770202
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  T CELL EPITOPES OF THE MAJOR ALLERGENS FROM
;    TITLE OF INVENTION:  DERMATOPHAGOIDES
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 STATE STREET, SUITE 510
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII TEXT
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/461,809
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/945,288
;      FILING DATE:  10 SEPTEMBER 1992
;      APPLICATION NUMBER:  US 580,655
;      FILING DATE:  11 SEPTEMBER 1990
;      APPLICATION NUMBER:  US 458,642
;      FILING DATE:  13 FEBRUARY 1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MANDRAGOURAS, AMY E.
;      REGISTRATION NUMBER:  36,207
;      REFERENCE/DOCKET NUMBER:  IPC-010CC (IMI-024)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  129 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc feature
;      LOCATION:  47
;      OTHER INFORMATION:  /label=Xaa is Thr or Ser
;    FEATURE:
;      NAME/KEY:  misc feature
;      LOCATION:  114
;      OTHER INFORMATION:  /label=Xaa is Asp or Asn
;    FEATURE:
;      NAME/KEY:  misc feature
;      LOCATION:  127
;      OTHER INFORMATION:  /label=Xaa is Ile or Leu
US-08-461-809-12

  Query Match             90.6%;  Score 627;  DB 1;  Length 129;
  Best Local Similarity   89.9%;  Pred. No. 3.5e-66;
  Matches  116;  Conservative    4;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||:||||||||:||||| |||||||||:||||||  ||||||||||||
Db          1 DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNXKTAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | |||||||||||||| |||| |||||||||||||||| ||||||||||:|| ||||||
Db         61 LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVMGDXGVLACA 120

Qy        121 IATHAKIRD 129
              ||||||  ||
Db        121 IATHAKXRD 129


RESULT 13
US-08-461-441-12
; Sequence 12, Application US/08461441
; Patent No. 5773002
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  T CELL EPITOPES OF THE MAJOR ALLERGENS FROM
;    TITLE OF INVENTION:  DERMATOPHAGOIDES
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 STATE STREET, SUITE 510
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;       CITY:  BOSTON
;       STATE:  MA
;       COUNTRY:  USA
;       ZIP:  02109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  ASCII TEXT
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/461,441
;       FILING DATE:
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/945,288
;       FILING DATE:  10 SEPTEMBER 1992
;       APPLICATION NUMBER:  US 580,655
;       FILING DATE:  11 SEPTEMBER 1990
;       APPLICATION NUMBER:  US 458,642
;       FILING DATE:  13 FEBRUARY 1990
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  MANDRAGOURAS, AMY E.
;       REGISTRATION NUMBER:  36,207
;       REFERENCE/DOCKET NUMBER:  IPC-010CC (IMI-024)
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 227-7400
;       TELEFAX:  (617) 227-5941
;   INFORMATION FOR SEQ ID NO:  12:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  129 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     FEATURE:
;       NAME/KEY:  misc feature
;       LOCATION:  47
;       OTHER INFORMATION:  /label=Xaa is Thr or Ser
;     FEATURE:
;       NAME/KEY:  misc feature
;       LOCATION:  114
;       OTHER INFORMATION:  /label=Xaa is Asp or Asn
;     FEATURE:
;       NAME/KEY:  misc feature
;       LOCATION:  127
;       OTHER INFORMATION:  /label=Xaa is Ile or Leu
US-08-461-441-12

  Query Match             90.6%;  Score 627;  DB 1;  Length 129;
  Best Local Similarity   89.9%;  Pred. No. 3.5e-66;
  Matches  116;  Conservative    4;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||:|||||||:|||||  |||||||||:||||||  ||||||||||||
Db          1 DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNXKTAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | |||||||||||||| |||| |||||||||||||||| ||||||||||:|| ||||||
Db         61 LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVMGDXGVLACA 120

Qy        121 IATHAKIRD 129
              ||||||  ||
Db        121 IATHAKXRD 129


RESULT 14
PCT-US93-08518-12
; Sequence 12, Application PC/TUS9308518
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  T CELL EPITOPES OF THE MAJOR ALLERGENS FROM
;    TITLE OF INVENTION:  DERMATOPHAGOIDES
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  LAHIVE & COCKFIELD
;       STREET:  60 STATE STREET, SUITE 510
;       CITY:  BOSTON
;       STATE:  MA
;       COUNTRY:  USA
;       ZIP:  02109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  ASCII TEXT
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US93/08518
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/945,288
;       FILING DATE:  10 SEPTEMBER 1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  MANDRAGOURAS, AMY E.
;       REGISTRATION NUMBER:  36,207
;       REFERENCE/DOCKET NUMBER:  IPC-010CC (IMI-024)
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 227-7400
;       TELEFAX:  (617) 227-5941
;   INFORMATION FOR SEQ ID NO:  12:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  129 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     FEATURE:
;       NAME/KEY:  misc feature
;       LOCATION:  47
;       OTHER INFORMATION:  /label=Xaa is Thr or Ser
;     FEATURE:
;       NAME/KEY:  misc feature
;       LOCATION:  114
;       OTHER INFORMATION:  /label=Xaa is Asp or Asn
;     FEATURE:
;       NAME/KEY:  misc feature
;       LOCATION:  127
;       OTHER INFORMATION:  /label=Xaa is Ile or Leu
PCT-US93-08518-12

  Query Match             90.6%;  Score 627;  DB 5;  Length 129;
  Best Local Similarity   89.9%;  Pred. No. 3.5e-66;
  Matches  116;  Conservative    4;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||:|||||||:|||||  |||||||||:||||||  ||||||||||||
Db          1 DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNXKTAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | |||||||||||||| |||| |||||||||||||||| ||||||||||:|| ||||||
Db         61 LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVMGDXGVLACA 120

Qy        121 IATHAKIRD 129
              ||||||  ||
Db        121 IATHAKXRD 129


RESULT 15
US-07-945-288-12
; Sequence 12, Application US/07945288
; Patent No. 5433948
;  GENERAL INFORMATION:
;    APPLICANT:  Thomas, Wayne R.
;    APPLICANT:  Chua, Kaw-Yan
;    TITLE OF INVENTION:  CLONING AND SEQUENCING OF ALLERGENS FROM
;    TITLE OF INVENTION:  DERMATOPHAGOIDES (HOUSE DUST MITES)
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
```

```
;      ADDRESSEE:  LAHIVE & COCKFIELD
;      STREET:  60 STATE STREET, SUITE 510
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII TEXT
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/945,288
;      FILING DATE:  19920910
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  580,655
;      FILING DATE:  11 SEPTEMBER 1990
;      APPLICATION NUMBER:  458,642
;      FILING DATE:  13 FEBRUARY 1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MANDRAGOURAS, AMY E.
;      REGISTRATION NUMBER:  P36,207
;      REFERENCE/DOCKET NUMBER:  IPC-010CC (IMI-024)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 227-7400
;      TELEFAX:  (617) 227-5941
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  129 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  misc feature
;      LOCATION:  47
;      OTHER INFORMATION:  /label=Xaa is Thr or Ser
;    FEATURE:
;      NAME/KEY:  misc feature
;      LOCATION:  113
;      OTHER INFORMATION:  /label=Xaa is Asp or Asn
;    FEATURE:
;      NAME/KEY:  misc feature
;      LOCATION:  127
;      OTHER INFORMATION:  /label=Xaa is Ile or Leu
US-07-945-288-12

  Query Match             89.9%;  Score 622;  DB 1;  Length 129;
  Best Local Similarity   89.1%;  Pred. No. 1.4e-65;
  Matches  115;  Conservative    5;  Mismatches    9;  Indels    0;  Gaps    0;

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              ||||||||||||||:||||||||:||||| |||||||||:||||||  ||||||||||||
Db          1 DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNXKTAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | |||||||||||||| |||| |||||||||||||||| ||||||||||:| :||||||
Db         61 LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVMGXDGVLACA 120

Qy        121 IATHAKIRD 129
              |||||| ||
Db        121 IATHAKXRD 129


Search completed: September  9, 2005, 15:10:16
Job time : 28 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 9, 2005, 15:06:59 ; Search time 393 Seconds
(without alignments)
129.470 Million cell updates/sec

Title: US-10-001-245C-36
Perfect score: 692
Sequence: 1 DQVDVKDCANHEIKEVLVPG.....VLGDNGVLACAIATHAKIRD 129

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1777461 seqs, 394431504 residues

Total number of hits satisfying chosen parameters: 1777461

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	692	100.0	129	14	US-10-001-245-36	Sequence 36, Appl
2	684	98.8	129	14	US-10-001-245-40	Sequence 40, Appl
3	684	98.8	129	14	US-10-001-245-46	Sequence 46, Appl
4	683	98.7	129	14	US-10-001-245-42	Sequence 42, Appl
5	683	98.7	129	14	US-10-001-245-44	Sequence 44, Appl
6	682	98.6	129	14	US-10-001-245-38	Sequence 38, Appl
7	665	96.1	129	14	US-10-001-245-48	Sequence 48, Appl
8	657	94.9	129	14	US-10-001-245-52	Sequence 52, Appl
9	657	94.9	129	14	US-10-001-245-54	Sequence 54, Appl
10	657	94.9	129	14	US-10-001-245-58	Sequence 58, Appl
11	656	94.8	129	14	US-10-001-245-56	Sequence 56, Appl
12	655	94.7	129	14	US-10-001-245-50	Sequence 50, Appl
13	648	93.6	129	14	US-10-001-245-94	Sequence 94, Appl
14	646	93.4	129	14	US-10-001-245-171	Sequence 171, App
15	643	92.9	129	14	US-10-001-245-169	Sequence 169, App
16	641	92.6	129	14	US-10-001-245-168	Sequence 168, App
17	638	92.2	129	14	US-10-001-245-170	Sequence 170, App
18	638	92.2	145	9	US-09-949-889-3	Sequence 3, Appli
19	635	91.8	129	14	US-10-001-245-90	Sequence 90, Appl
20	635	91.8	129	16	US-10-698-855-8	Sequence 8, Appli
21	635	91.8	136	16	US-10-799-514-17	Sequence 17, Appl
22	635	91.8	146	9	US-09-877-160-3	Sequence 3, Appli
23	635	91.8	146	10	US-09-847-208-80	Sequence 80, Appl
24	635	91.8	146	14	US-10-001-245-138	Sequence 138, App
25	635	91.8	146	16	US-10-809-689-20	Sequence 20, Appl
26	631	91.2	129	14	US-10-001-245-167	Sequence 167, App
27	629	90.9	128	14	US-10-001-245-172	Sequence 172, App
28	629	90.9	129	12	US-09-957-806A-8	Sequence 8, Appli
29	621	89.7	129	9	US-09-949-889-4	Sequence 4, Appli
30	596	86.1	146	14	US-10-001-245-173	Sequence 173, App
31	594	85.8	138	14	US-10-001-245-174	Sequence 174, App
32	592	85.5	129	14	US-10-001-245-175	Sequence 175, App
33	592	85.5	146	10	US-09-847-208-74	Sequence 74, Appl
34	592	85.5	146	16	US-10-809-689-28	Sequence 28, Appl
35	590	85.3	129	14	US-10-001-245-176	Sequence 176, App
36	588	85.0	129	12	US-09-957-806A-7	Sequence 7, Appli
37	576	83.2	135	14	US-10-001-245-178	Sequence 178, App
38	575	83.1	145	14	US-10-001-245-177	Sequence 177, App
39	365	52.7	73	16	US-10-799-514-16	Sequence 16, Appl
40	365	52.7	159	16	US-10-799-514-23	Sequence 23, Appl
41	352.5	50.9	153	16	US-10-799-514-22	Sequence 22, Appl
42	348	50.3	72	16	US-10-799-514-15	Sequence 15, Appl
43	272.5	39.4	126	9	US-09-860-793-1	Sequence 1, Appli
44	272.5	39.4	143	9	US-09-860-793-3	Sequence 3, Appli
45	251	36.3	125	16	US-10-698-855-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-10-001-245-36
; Sequence 36, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
; APPLICANT: HOLM, Jens
; APPLICANT: IPSEN, Henrik
; APPLICANT: LARSEN, Jorgen N.
; APPLICANT: SPANGFORT, Michael D.
; TITLE OF INVENTION: No. US20030175312A1el mutant allergens
; FILE REFERENCE: 4305/1H942-US2
; CURRENT APPLICATION NUMBER: US/10/001,245
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/298,170
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/249,361
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-36

Query Match 100.0%; Score 692; DB 14; Length 129;
Best Local Similarity 100.0%; Pred. No. 4.6e-73;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120

Qy         121 IATHAKIRD 129
               |||||||||
Db         121 IATHAKIRD 129


RESULT 2
US-10-001-245-40
; Sequence 40, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
;  APPLICANT: HOLM, Jens
;  APPLICANT:  IPSEN, Henrik
;  APPLICANT:  LARSEN, Jorgen N.
;  APPLICANT:  SPANGFORT, Michael D.
;  TITLE OF INVENTION: No. US20030175312A1el mutant allergens
;  FILE REFERENCE: 4305/1H942-US2
;  CURRENT APPLICATION NUMBER: US/10/001,245
;  CURRENT FILING DATE:  2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/298,170
;  PRIOR FILING DATE: 2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/249,361
;  PRIOR FILING DATE: 2000-11-16
;  NUMBER OF SEQ ID NOS: 217
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-40

  Query Match             98.8%;  Score 684;  DB 14;  Length 129;
  Best Local Similarity   98.4%;  Pred. No. 4e-72;
  Matches  127;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LEVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120

Qy        121 IATHAKIRD 129
               |||||||:|
Db        121 IATHAKIQD 129


RESULT 3
US-10-001-245-46
; Sequence 46, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
;  APPLICANT: HOLM, Jens
;  APPLICANT:  IPSEN, Henrik
;  APPLICANT:  LARSEN, Jorgen N.
;  APPLICANT:  SPANGFORT, Michael D.
;  TITLE OF INVENTION: No. US20030175312A1el mutant allergens
;  FILE REFERENCE: 4305/1H942-US2
;  CURRENT APPLICATION NUMBER: US/10/001,245
;  CURRENT FILING DATE:  2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/298,170
;  PRIOR FILING DATE: 2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/249,361
;  PRIOR FILING DATE: 2000-11-16
;  NUMBER OF SEQ ID NOS: 217
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-46

  Query Match             98.8%;  Score 684;  DB 14;  Length 129;
  Best Local Similarity   98.4%;  Pred. No. 4e-72;
  Matches  127;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DQVDVKDCANHEIKKVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120

Qy        121 IATHAKIRD 129
               |||||||:|
Db        121 IATHAKIQD 129


RESULT 4
US-10-001-245-42
; Sequence 42, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
;  APPLICANT: HOLM, Jens
;  APPLICANT:  IPSEN, Henrik
;  APPLICANT:  LARSEN, Jorgen N.
;  APPLICANT:  SPANGFORT, Michael D.
;  TITLE OF INVENTION: No. US20030175312A1el mutant allergens
;  FILE REFERENCE: 4305/1H942-US2
;  CURRENT APPLICATION NUMBER: US/10/001,245
;  CURRENT FILING DATE:  2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/298,170
;  PRIOR FILING DATE: 2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/249,361
;  PRIOR FILING DATE: 2000-11-16
;  NUMBER OF SEQ ID NOS: 217
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-42

  Query Match             98.7%;  Score 683;  DB 14;  Length 129;
  Best Local Similarity   98.4%;  Pred. No. 5.3e-72;
  Matches  127;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSKTAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120

Qy        121 IATHAKIRD 129
               |||||||:|
Db        121 IATHAKIQD 129


RESULT 5
US-10-001-245-44
; Sequence 44, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
;  APPLICANT: HOLM, Jens
;  APPLICANT:  IPSEN, Henrik
;  APPLICANT:  LARSEN, Jorgen N.
;  APPLICANT:  SPANGFORT, Michael D.
;  TITLE OF INVENTION: No. US20030175312A1el mutant allergens
;  FILE REFERENCE: 4305/1H942-US2
;  CURRENT APPLICATION NUMBER: US/10/001,245
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;  CURRENT FILING DATE:  2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/298,170
;  PRIOR FILING DATE: 2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/249,361
;  PRIOR FILING DATE: 2000-11-16
;  NUMBER OF SEQ ID NOS: 217
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-44

  Query Match             98.7%;  Score 683;  DB 14;  Length 129;
  Best Local Similarity   98.4%;  Pred. No. 5.3e-72;
  Matches  127;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||
Db          1 DQVDVKDCANHEIKEVLVPGCHGSEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120

Qy        121 IATHAKIRD 129
              |||||||:|
Db        121 IATHAKIQD 129


RESULT 6
US-10-001-245-38
; Sequence 38, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
;  APPLICANT: HOLM, Jens
;  APPLICANT:  IPSEN, Henrik
;  APPLICANT:  LARSEN, Jorgen N.
;  APPLICANT:  SPANGFORT, Michael D.
;  TITLE OF INVENTION: No. US20030175312A1el mutant allergens
;  FILE REFERENCE: 4305/1H942-US2
;  CURRENT APPLICATION NUMBER: US/10/001,245
;  CURRENT FILING DATE:  2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/298,170
;  PRIOR FILING DATE: 2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/249,361
;  PRIOR FILING DATE: 2000-11-16
;  NUMBER OF SEQ ID NOS: 217
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-38

  Query Match             98.6%;  Score 682;  DB 14;  Length 129;
  Best Local Similarity   98.4%;  Pred. No. 6.9e-72;
  Matches  127;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPKSENVVVTVKVLGDNGVLACA 120

Qy        121 IATHAKIRD 129
              |||||||:|
Db        121 IATHAKIQD 129


RESULT 7
```

```
US-10-001-245-48
; Sequence 48, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
;  APPLICANT: HOLM, Jens
;  APPLICANT:  IPSEN, Henrik
;  APPLICANT:  LARSEN, Jorgen N.
;  APPLICANT:  SPANGFORT, Michael D.
;  TITLE OF INVENTION: No. US20030175312A1el mutant allergens
;  FILE REFERENCE: 4305/1H942-US2
;  CURRENT APPLICATION NUMBER: US/10/001,245
;  CURRENT FILING DATE:  2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/298,170
;  PRIOR FILING DATE: 2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/249,361
;  PRIOR FILING DATE: 2000-11-16
;  NUMBER OF SEQ ID NOS: 217
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-48

  Query Match             96.1%;  Score 665;  DB 14;  Length 129;
  Best Local Similarity   96.9%;  Pred. No. 6.9e-70;
  Matches  125;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIHSGKPFQLEALFEANQNSATAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              |||||||||||||:|| ||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSVDVPGIDPNACNYMKCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120

Qy        121 IATHAKIRD 129
              |||||||||
Db        121 IATHAKIRD 129


RESULT 8
US-10-001-245-52
; Sequence 52, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
;  APPLICANT: HOLM, Jens
;  APPLICANT:  IPSEN, Henrik
;  APPLICANT:  LARSEN, Jorgen N.
;  APPLICANT:  SPANGFORT, Michael D.
;  TITLE OF INVENTION: No. US20030175312A1el mutant allergens
;  FILE REFERENCE: 4305/1H942-US2
;  CURRENT APPLICATION NUMBER: US/10/001,245
;  CURRENT FILING DATE:  2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/298,170
;  PRIOR FILING DATE: 2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/249,361
;  PRIOR FILING DATE: 2000-11-16
;  NUMBER OF SEQ ID NOS: 217
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-52

  Query Match             94.9%;  Score 657;  DB 14;  Length 129;
  Best Local Similarity   95.3%;  Pred. No. 6e-69;
  Matches  123;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIHSGKPFQLEALFEANQNSATAKIEIKASIDG 60
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```
Qy          61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
               | ||||||||||||:|| ||||||||||||||||||||||||||||||||||||||||||||
Db          61 LEVDVPGIDPNACNYMKCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120

Qy         121 IATHAKIRD 129
               |||||||:|
Db         121 IATHAKIQD 129


RESULT 9
US-10-001-245-54
; Sequence 54, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
;  APPLICANT: HOLM, Jens
;  APPLICANT:  IPSEN, Henrik
;  APPLICANT:  LARSEN, Jorgen N.
;  APPLICANT:  SPANGFORT, Michael D.
;  TITLE OF INVENTION: No. US20030175312A1el mutant allergens
;  FILE REFERENCE: 4305/1H942-US2
;  CURRENT APPLICATION NUMBER: US/10/001,245
;  CURRENT FILING DATE:  2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/298,170
;  PRIOR FILING DATE: 2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/249,361
;  PRIOR FILING DATE: 2000-11-16
;  NUMBER OF SEQ ID NOS: 217
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-54

  Query Match             94.9%;  Score 657;  DB 14;  Length 129;
  Best Local Similarity   95.3%;  Pred. No. 6e-69;
  Matches  123;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIHSGKPFQLEALFEANQNSATAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
               | ||||||||||||:|| ||||||||||||||||||||||||||||||||||||||||||||
Db         61 LEVDVPGIDPNACNYMKCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120

Qy        121 IATHAKIRD 129
               |||||||:|
Db        121 IATHAKIQD 129


RESULT 10
US-10-001-245-58
; Sequence 58, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
;  APPLICANT: HOLM, Jens
;  APPLICANT:  IPSEN, Henrik
;  APPLICANT:  LARSEN, Jorgen N.
;  APPLICANT:  SPANGFORT, Michael D.
;  TITLE OF INVENTION: No. US20030175312A1el mutant allergens
;  FILE REFERENCE: 4305/1H942-US2
;  CURRENT APPLICATION NUMBER: US/10/001,245
;  CURRENT FILING DATE:  2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/298,170
;  PRIOR FILING DATE: 2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/249,361
;  PRIOR FILING DATE: 2000-11-16
;  NUMBER OF SEQ ID NOS: 217
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-58

  Query Match             94.9%;  Score 657;  DB 14;  Length 129;
  Best Local Similarity   95.3%;  Pred. No. 6e-69;
  Matches  123;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              |||||||||||||||:|||||||||||||  ||||||||||||||||||||||||||||||
Db          1 DQVDVKDCANHEIKKVLVPGCHGNEPCIIHSGKPFQLEALFEANQNSATAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
               |||||||||||||:|| ||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSVDVPGIDPNACNYMKCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120

Qy        121 IATHAKIRD 129
               |||||||:|
Db        121 IATHAKIQD 129


RESULT 11
US-10-001-245-56
; Sequence 56, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
;  APPLICANT: HOLM, Jens
;  APPLICANT:  IPSEN, Henrik
;  APPLICANT:  LARSEN, Jorgen N.
;  APPLICANT:  SPANGFORT, Michael D.
;  TITLE OF INVENTION: No. US20030175312A1el mutant allergens
;  FILE REFERENCE: 4305/1H942-US2
;  CURRENT APPLICATION NUMBER: US/10/001,245
;  CURRENT FILING DATE:  2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/298,170
;  PRIOR FILING DATE: 2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/249,361
;  PRIOR FILING DATE: 2000-11-16
;  NUMBER OF SEQ ID NOS: 217
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-56

  Query Match             94.8%;  Score 656;  DB 14;  Length 129;
  Best Local Similarity   95.3%;  Pred. No. 7.9e-69;
  Matches  123;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              |||||||||||||||||||||||:|||||  ||||||||||||||||||||||||||||||
Db          1 DQVDVKDCANHEIKEVLVPGCHGSEPCIIHSGKPFQLEALFEANQNSATAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
               |||||||||||||:|| ||||||||||||||||||||||||||||||||||||||||||||
Db         61 LSVDVPGIDPNACNYMKCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120

Qy        121 IATHAKIRD 129
               |||||||:|
Db        121 IATHAKIQD 129


RESULT 12
US-10-001-245-50
; Sequence 50, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
;  APPLICANT: HOLM, Jens
;  APPLICANT:  IPSEN, Henrik
;  APPLICANT:  LARSEN, Jorgen N.
;  APPLICANT:  SPANGFORT, Michael D.
;  TITLE OF INVENTION: No. US20030175312A1el mutant allergens
```

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;  FILE REFERENCE: 4305/1H942-US2
;  CURRENT APPLICATION NUMBER: US/10/001,245
;  CURRENT FILING DATE:  2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/298,170
;  PRIOR FILING DATE: 2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/249,361
;  PRIOR FILING DATE: 2000-11-16
;  NUMBER OF SEQ ID NOS: 217
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-50

  Query Match             94.7%;  Score 655;  DB 14;  Length 129;
  Best Local Similarity   95.3%;  Pred. No. 1e-68;
  Matches  123;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIHSGKPFQLEALFEANQNSATAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              |||||||||||||:|| ||||||||||||||||||||| ||||||||||||||||||||
Db         61 LSVDVPGIDPNACNYMKCPLVNGQQYDIKYTWNVPKIAPKSENVVVTVKVLGDNGVLACA 120

Qy        121 IATHAKIRD 129
              |||||||:|
Db        121 IATHAKIQD 129


RESULT 13
US-10-001-245-94
; Sequence 94, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
;  APPLICANT: HOLM, Jens
;  APPLICANT:  IPSEN, Henrik
;  APPLICANT:  LARSEN, Jorgen N.
;  APPLICANT:  SPANGFORT, Michael D.
;  TITLE OF INVENTION: No. US20030175312A1el mutant allergens
;  FILE REFERENCE: 4305/1H942-US2
;  CURRENT APPLICATION NUMBER: US/10/001,245
;  CURRENT FILING DATE:  2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/298,170
;  PRIOR FILING DATE: 2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/249,361
;  PRIOR FILING DATE: 2000-11-16
;  NUMBER OF SEQ ID NOS: 217
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 94
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-94

  Query Match             93.6%;  Score 648;  DB 14;  Length 129;
  Best Local Similarity   93.8%;  Pred. No. 6.9e-68;
  Matches  121;  Conservative    2;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||:||||||||:||||| |||||||||||||||| ||||||||||||
Db          1 DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEALFEANQNSKTAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | |||||||||||||| |||| ||||||||||||||||| |||||||||||||||||||
Db         61 LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVLGDNGVLACA 120

Qy        121 IATHAKIRD 129
              |||||||||
Db        121 IATHAKIRD 129


RESULT 14
US-10-001-245-171
; Sequence 171, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
;  APPLICANT: HOLM, Jens
;  APPLICANT:  IPSEN, Henrik
;  APPLICANT:  LARSEN, Jorgen N.
;  APPLICANT:  SPANGFORT, Michael D.
;  TITLE OF INVENTION: No. US20030175312A1el mutant allergens
;  FILE REFERENCE: 4305/1H942-US2
;  CURRENT APPLICATION NUMBER: US/10/001,245
;  CURRENT FILING DATE:  2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/298,170
;  PRIOR FILING DATE: 2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/249,361
;  PRIOR FILING DATE: 2000-11-16
;  NUMBER OF SEQ ID NOS: 217
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 171
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-171

  Query Match             93.4%;  Score 646;  DB 14;  Length 129;
  Best Local Similarity   93.0%;  Pred. No. 1.2e-67;
  Matches  120;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
              ||||||||||||||:||||||||:||||| |||||||||||||||| ||||||||||||
Db          1 DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEALFEANQNSKTAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
              | |||||||||||||| |||| ||||||||||||||||| ||||||||||:|||||||||
Db         61 LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVMGDNGVLACA 120

Qy        121 IATHAKIRD 129
              |||||||||
Db        121 IATHAKIRD 129


RESULT 15
US-10-001-245-169
; Sequence 169, Application US/10001245
; Publication No. US20030175312A1
; GENERAL INFORMATION:
;  APPLICANT: HOLM, Jens
;  APPLICANT:  IPSEN, Henrik
;  APPLICANT:  LARSEN, Jorgen N.
;  APPLICANT:  SPANGFORT, Michael D.
;  TITLE OF INVENTION: No. US20030175312A1el mutant allergens
;  FILE REFERENCE: 4305/1H942-US2
;  CURRENT APPLICATION NUMBER: US/10/001,245
;  CURRENT FILING DATE:  2001-11-15
;  PRIOR APPLICATION NUMBER: US 60/298,170
;  PRIOR FILING DATE: 2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/249,361
;  PRIOR FILING DATE: 2000-11-16
;  NUMBER OF SEQ ID NOS: 217
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 169
;   LENGTH: 129
;   TYPE: PRT
;   ORGANISM: Dermatophagoides pteronyssinus
US-10-001-245-169

  Query Match             92.9%;  Score 643;  DB 14;  Length 129;
  Best Local Similarity   92.2%;  Pred. No. 2.7e-67;
  Matches  119;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 DQVDVKDCANHEIKEVLVPGCHGNEPCIIGRGKPFQLEALFEANQNSATAKIEIKASIDG 60
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                ||||||||||||||:||||||||:|||||| |||||||||:|||||||| ||||||||||||
Db          1 DQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNSKTAKIEIKASIDG 60

Qy         61 LSVDVPGIDPNACHYMNCPLVNGQQYDIKYTWNVPKIAPNSENVVVTVKVLGDNGVLACA 120
                | ||||||||||||||| |||| |||||||||||||||| ||||||||||:|||||||||
Db         61 LEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVIGDNGVLACA 120

Qy        121 IATHAKIRD 129
                |||||||||
Db        121 IATHAKIRD 129


Search completed: September  9, 2005, 15:20:09
Job time : 393 secs
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